

FIGURE 1

CGGACGCGTGGGTGCGAGGCCAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGAC
 CTGGTGCACCCACCA**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCCCAAGGCTCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
 ATGGCTGTTAAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTAAAAATT
 GATCAGATGGGAAGATGTTTGTGTCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCAAAGCATCTTGCTTGGTGTCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATGTGGGAGGCCCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTGTGTCTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGGCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTCTTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAATAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAA**TG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAAATCTTGTTTAAATGGGGCAGATATGC
 ATTAATAAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAAATAATGCAGT
 AATCTCTCCCCAATAAGCACACATTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAATAAGTTTGTGTATGAGAAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTTGCATATTTTTTTGGAGT
 GCAGAAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTATTGATTA
 GTGAGGAGCCAGTAAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCAATT
 GCTGAACCTTAACAAAAGTTCATCCTGAAACAGGCACAGGTGATGCATCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAAATATAGATGTGGTCATGTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCTTGATGGAATTATATATGTGTGTTTTACTTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTGCTTTTCCAG
 AATACAAAAGTATACATCATG

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FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTFVLMNFMMRGSSWVTIGVTFAMVVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLS IYMDTLNIFMRVATMLATGGNRKK

FIGURE 3

GAAGGCTGCCTCGTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGCTCTCCGCCTTCTGCAT
 CGCGGCTCTCGCGGCTTCCACCTAGACACCTAACAGTCGCGGGAGCCGGCCGCTCGTAGAGG
 GTGCGGCACGGGAGTCCGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCCGAAGATGTCGG
 ACATCCGAGACTGGTTCAGGAGCATCCCGCGCATACGCGCTATTGGTTTCGCCGCCACCGTC
 CGCGTCCCTTGGTCCGCAAACTCGGCCCTCATCAGCCGCGCTACCTCTTCTCTGGCCCGA
 AGCCTTCCCTTATCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 GTCCAGGAATCGATTATTTCTTATTTGGTCAATTTATATTTCTTATATCAGTATCTACGGGA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCTCTGTATCA
 GTTCTGATCTTTATGCTCGGCCACGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
 ACACGATTTAAGGCCCTGCTATTTACCCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTGGGTAATCAATGAGCTTATTTGGAAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCAATGGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTGTACCCGCTGG
 CTGCCGATAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGAGGCCGAGACAACCTGGGCCAGGGCTTTCGACTTGGAGACC
 AGTGAAGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG
 CACTTAACAACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTT
 AGTACGAGACAAGTTTCTTAAATCCCGAAGAAAATATAAGTGTCCACAACTTTTCCAGAT
 TCTCAATCACTCTTACTGCTGTGAAGACAATAACCACTGTGCAAAATGCAAAATGAC
 TACATTTTTTGGTGTCTTCTCTCTCCCTTTCCGCTGAATAATGGGTTTATAGCGGGTCTCT
 AATCTGCTGCATTTGAGCTGGGGCTGGGTACCAAAACCCCTTCCCAAAGGACCTTATCTCTT
 TCTTGACACATGCTCTCTCCACCTTTTCCAAACCCACATTTGCAACTGAAAAGGTTG
 CCAATAAAATTTGCTTGGCCCTTGACAGGTTCTGTATTTATTGACTTTTCCAAAGGCTGGT
 ACAACAAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAACTGTTCACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCGTTTTCTCAGCTTTTGGAAATGCTCGACTGACATCCGTTGTT
 AACCGTTTGGCAGCTTTCAGATATTTTTATAAAAAAAGTACCCTGAGTTCATGAGGGCCA
 CAGATTTGGTATTTAATGACATACGAGGTTGGTGTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGGGGATGACCCCT
 TTTGCGTTTCAATGTAGGCCCTACTGGCTTTGTGAGCTGGAGTACTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATG
 ATTCCCAATTTCAATCTCATTCTGGATATGTGTTCAATGAGTAAAGGAGGAGAGACCCCTCATA
 CGCTATTTAAATGTCACTTTTTTGGCTATCCCCCGTTTTTGGTGTGTTTCAATTAATGT
 GAGGAAGGCCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTGAAATGGCTTAGAATCATTTGGGTTTGAGGGTGTGTTA
 TTTTGAGTCAATGAATGTACAAGCTCTGTAATCAGACCACTTAATACCCACCTTTTTTT
 TCGTAGTGGGCTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCA
 TGCGTTTTACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACTTTTGGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTCTT
 TTCAGGAACAATTTGCTCTAACAGTATGACTATCTTTCCCACTCTTAAACAGTGTGAT
 GTCTGTTATCTAGGAAATGAGAGTTGGCAACCAACTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTAAATTTATATGATAAAATAGGTGGGGAGACTGAACTTAACTGTGTA
 TGTTTTGTTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTA
 CCAATTAATGTTCAAGCTACACTATTGTACAGGCGTGAGACTCATTGTATGTATAAGAAAT
 TTTCTGACAGTGAGTGACCCGAGTCTCTGGTGTACCCCTCTTACAGTCAGCTGCCTGCGAG
 CAGTCATTTTTTCTAAAGGTTTACAAGTATTTAGAATTTTCACTGAGGGCAAAATGTTCT
 ATAAGGTTATTTCCCTTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAAGGCCAAATA
 TGACAGTGGATTCTCTTTACAAATGGAATAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTAAACTAATCCTTTTTATTGGTAAAAATTTGAAATTAATGTGCACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGGT
 CTTTGTGGCCCAAAGGCTTAACCGGGTCCGCGGCTCTGGCTAGGGATCTTCCCCGTGGC
 CCTTTGGGGCGG**GATGG**CTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAAACAGGAAGAGATGAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAAACAAGAGCCACAGTGCACTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAAATTAAGAACAATTTAACAAATGGAAGTCAAATTTGCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEEDVEVWVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLPDCLTDGSDVVSdleHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTAGTATGTCGCTTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC
 AGTGGAAATGGAAGAACAGTGCTGTAGTCATCCTGTAATATGCTCTTGTCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAAGT
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTCGCT
 TTCTTTATTTCTGGATAACTGATTGTCTTCTATGTCCTGTCTTCTCAACAGCCATG
 GCTGTTATCTTCAAAATTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGCTGAA
 GAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCT
 TGACTGCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCAGCATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCCTTCTTTTCAAGAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC
 ACATCCGCTCTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCAGTGAAGAGCATCTTCTATACA
 GAACAGCAAACCTCATTTCTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCTTCAAGAGA
 GTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTCCAGGGCCTTTCAGTGGCTTTTCATTCTGAAGTTCTCGGATTA
 CATGTTCCAGTCTTGATGGCCAGGTTACCACTGTGCTATTATCAACAAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTCTTGGAAAGCCCATCAGTCTCTCTCTATA
 TTTATTTATGAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAAGTATGAAAGACTTA
 CCAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTGAACCTTATTTTCACATTTTCAGTGTTTGTAATATTTATCTTTTCACTTTTGATA
 AACCAGAAATGTTTCAAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCAAGGCTAAGAAATCTAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAATCTGTAATAATCATGTTAGCTATAGCTTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTAGTTTCAATGCGCAAGT
 CTCCCTTTTAAACATTTATAAAGCTAGGTTGTCTCTTGAAATTTGAGGCGCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAATATTTTGGCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAAATTTAATTTTTAGAAATTCATGGGAATTTGGATTTTTGT
 AATAATCTTTTGTATTTTAAACATTTGGTTCCCTAGTCACCATAGTTACCCTTGTATTTTA
 AGTCATTTAAACAAGCCAGGTTGGGCTTTTTCTCCTCAGTTTGGAGAGAAAAATCTTGAT
 GTCATTACTCTGAATTATACATTTTGGAGAATAAGAGGGCATTTTATTTTATAGTTACT
 AATTTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAAATGCTGGCTTCAAGATCATAC
 CAGATTGTGCTGAGCTGATGCTTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCAAAAATAGAAGACC
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACTTAAAGTGATGCTGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAAAACAAGTGACTTGTCTAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATACTGTAATATGAGCTTATGGTGT
 CATTCTCAGAACTTATACATTTCTGCTCTCTTCTCTCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATAAATTCATTGTGATATCCCAATAATATGACTGGCAAGAAATG
 GTGGAATTTGTAATTAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIPIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDFAFF
 SPSNSCLLFRSECPKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFVSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLISIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCAATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAAGTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGATAGTGTCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGCCCTGCGGGGCGAGAGGAGCAT
 CCCGTCTACCAAGTCCCAAGCGGCGTGGCCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAAGCATCCTCCAAAGCACTGAACGCCCGGCCA
 GGTGAAGAAAGAACCAGAAAAGAAGAAACAACAGTTGTCTGTTTGAACAAGCTTTGGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
 CTATTGGATGGTGGCTCAGGTGGGCCCTTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATACAGACCCCTGGTGGGCCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTATTGCCTACTTCCCTC
 ATCTGGTTCTGTCGCCGACTTCCCAACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCAGTGTTTCCATGTTCCCTACTCGGCTCTCCACCATGTTTATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAACATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTACAAAAGTGCCAAACCATACACATGGCACCACCTTCACAC
 AGGGAACGCAAAAGGCATACCTGTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGCCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCT
 ATTACTGGCTTCCCTTCCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAACTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTCCCATCTGGCAGTGGTCTTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCTTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTACCAAGTTTGCCTCTGGAGTGT
 ACTGGGCATTTCTACCCCTCAGTCTGGACTTTGCAGGTTACAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTTCTCATCTCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGGCGGAGAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCTAGGGCCCCGCCAGTTGCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCCAGGACACTTGCTGTCTCACTGTGGGGCGGCTGCTCTG
 TGGCCTCCTGCTCCCTCTGCCTGCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAACCCTTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAGCTGGAAGC

FIGURE 12

MWLRWALS LPPSSCLWAEFGMP SQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGTCF SIA SLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIIICAV
ILILGVREQREP YEAAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

12/330 12/330 12/330

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGCTGTATCTATATAATCTGT
GCTGTTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGTTTCTTGACCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGACTTGGAATACTGAGTTGTTTAGG
 ACTTTCATTGTGGCAAACCTCCAGAAAAACAACCCTTTTGTCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTCGACAGTGGCAATTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
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FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTA AACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCTCCTTCTGGTCTTCGCGCGCTGCAC
 CTTTCGCTTGTACTTGTGCTGTCGACGCGACTGCCCGGGCGGAGACTGGGCTCCACCAGAG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCTGAAATGTTTTAGCTGGTGCTT
 TGTTTGGGCCATGGCTGGGGCTTCTGTGTGTGTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAAATTCATCTGTGT
 GCAGACAGGGTCCATCCTGTGAACCTTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTCATTAATAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGACTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCCCTAAAGCCCCCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGAGTAAGCCAAGATCACACCCTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEEAGGRSLWFFSDLAELRELSVLREYR
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLCCVLTSGATCCYLLSS
IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF
FSVLIGLIPYNFICVQTSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCGCTCAGTTGTGATCAAGGGACACGTGGTTCCGAACGCCAGCTCAGAA
 TAGGAAAAATAACTTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAGAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGTCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAAATAAGGGAGTTCTCTGCATGGGGTGATGAAGACAGACCTTTC
 CAGACTTGGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCACTGGCTGTGCCAGAAACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGTGATCAAGACGGGAAAGCCCTGTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTCTCTGAGCGGTGGTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTCTGTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCAACCAGAACCTGTTGTGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGCTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLEKNEPQRPPQYPLLIIVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPV
FTHLPFFKDasLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDTAFSEL

FIGURE 21

CCACGGTGTCGGTTCTTCGCCCGCGGCAGCTGTCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTCCGAACGCGCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTATC
AGACAGCTGCTGGAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGGTGGTG
 CCACTGGTGGCAGCGTCTAGACCGTGCCCTATGAGCGCTGGGGCTGCAAGTGGGGACTGCC
 CTCCCTGCCACCCAAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CTTCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACTGTCAGCTCCGAATTCGAAATG
 GACACGCTATGCTAAGAGCGCAGCACTTATGTACAGTTTCTGGAATGCCCTGCTATGACATGCT
 TATGAGCACTGGGCAAGCGCGCCAGTGGGAGCGCGCCAGAGTCGTGGGGCTTCCAGGAGC
 TGTGCTGGAACTCGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACCTGGGGGGCGCTGTGGCGCCAGAT
 CGCCAGCCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACACTGTCCA
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTTGACACCCACCGAGGAGGC
 CTCACTGCTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCACCCAGGTTGCTGCAGG
 AGGACACGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCGAGCAACTG
 GATGAGCAGCGTGAGAAGCTGGTGTCTGGCGCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCAGGGCTGCTGGAGGTCAACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAACACCGAGGAGGCGATCGGCTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGAG
 GTCCACTTGGCGCTTTCAACCTGCGCCGTTGACGACTTGAGCTCTTCTTTATCGATCAGGC
 CAACTACTTCTCAACTTCCCATGCAAGTGGGCGAGCCAGCTCATCTCTCAAGCCAGCA
 CTCGAGACCCAGCTGGCCCCATCCACCCCATACCCAGGTACGGAACCAAGGTGTACTG
 TGCTCTGCGCCCTACGGCCCCCTCTCAAGGCTTACCAAGCAGCCGCTCCCCAGGCTGTGTTG
 GCTGCGTGGCTCAGGCGCTTACCAGAAATGGGTACAGCGTGAGATATCCAACCTCTGAGTACT
 TGATGCAACTCAACACCATTTGCGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTG
 CCTGGGTCTGTCAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCGCTGTCCG
 GGACCTCTGAAGCCCTCGGTGGTGAACCCCAAGCATGCGCACTCGTGAGGGAGAAGT
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATGACAAGTTCCACTATGGCACCCTACTCC
 AATGACGAGCGTGATGCACCTACTCTATCGCGGTGGAGCCCTTCACTCCCTCAGCTGCCA
 GCTGCAAGTGGCGCTTTGACTGCTCCGACCGGCACTTCCATCGGTGGCGGAGCTGGC
 AGGCACGCTGGAGGCTGCGGATGTGAAGGAGCTCATCCCGAATTTCTTACTTTCTTCT
 GACTTCTGGAGAACCAGAACGGTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGT
 AGGCGATGTGGTGCTTACCCCTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCGCCGAGGAGGCCCTCAATGTCTTCTATTATGACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGAGACTCCTCTGTGAGTGTGAAGGAGCCACATCCAACCTCGGCTTCA
 CCTGAGGAAGCAGCCCATCGCTTGCACGCTGGACACTAATCACTCAGCTAGCATCTCCAGCA
 GCTTGAAGCAACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGCCAGTGGGCTGTGGGGA
 CCCACAGCTGGTTGGCTTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAGAGCCCC
 ACCATGGGCGCCACAAGCAGCAGCACTGCTGAGTGGCCGCTGGGTGCCAGGAGTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGATGGAAGCTGCTATTGAGCGGTGGCCACTGGG
 ATGGCAGCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCCTGCACCTGGACACTGTGGCACTCACTCATCTCAGGCTCCCG
 GGACACCACTGCTGAGTGGTGGCGGCTCCCTGCATCAGGTGGTCTGTGCTAGGCGCTGGCAG
 CAAAGCCTGTGAGGCTCCTGTATGGGCACTGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACCTTGACATGGCTGTGTCTGGATCTGAGGATGGAACCTGTATCATACACTGTACCGCG
 CGGACAGTTTGTAGGGGCACTACGGCTCTGGGTGCCACATTTCCCTGGACCTATTTTCCACC
 TGGCATTTGGGCTGAGGCGCAGATTGTGGTACAGAGCTCAGCGTGGGAACGCTCTGGGGCC
 CAGGTCACTACTCTTGCACCTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGCCCTCT
 GGCAGAGCAGCTACAGCGCTGACGGTGACAGAGGACTTTGTGTTGCTGGGACCGCCAGT
 GCGCCCTGCACATCTCCAACATAACACACTGCTCCCGGGCGCGCTCCTTGTGCCATGAAG
 GTGGCCATCCGCAAGCTGGCCGTGACCAAGGAGCGCAGCGCTGCTGGTGGGCTGGAGGA
 TGGAAGCTCATCTGCTGGTGGTGCAGGGGCGAGCGCTCTGAGGTGGCAGCAGGCAAGTTCGCGC
 GGAAGCTGTGGCGGTGTGTCGCGCGCATCTCCAGGTTCTCTCGGAGAGACGGAATAACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCCGCGAGCGCTG
 GCGCGGAGGCCCCCGCAAGTTCGCGGGGAACACCCCGGGGTGGGCAAGCTCAGGCGGTGA
 GCGGGGCCACCTCTGCCAGCTCAGGATTGGCGGGCATGTTACCCCTCAGGAGTTGGCG
 GCGGAGTCCCGCCCTCGCCGGCTGAGGGGCGCGCTGAGGGCCAGCTGCGGCTGT

FIGURE 23

MSQFEMDTYAKSHDMLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRKLKLVFN
 HHFDPHLEASALRNLNLEGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEIGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLKSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSAVAAWQARLESPADVKEKIP
 EFFFYFPDFLENQNGFDLGLCLQLTNEKVGDVVLPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTRQLLSSGPVWPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGRDTCMVWRLHLQGGLSVGLAPKPVQVLYGHGAVS
 CVAISTELDMAVSGSEDTGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVTVSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQFSEVRSSQFARKLWRSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

CGGACGCGTGGGCGGACGCGTGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCAT
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATATGGGGTCTTGGGGCTCTTC
TGGACCCTTAACTGGGTACTGGCCCTGGGGCAATGCGTCTCTCGTGGAGCCCTTGGCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCCTGTGCAG
ATAGCCCGGGTCACTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCCTCTGGTGCTCGGAAAAAATTTATCAAGTTCC
TAACCCGCAATGCATACATCATGATCCGCATCTACGGGAAGAATTTCTGTCTCAGCCAAA
AATGCGTCTACTGCTACTCATGCGAAACATTTGTCAGGGTGGTGCTCTTGACAAGAATGCACAGA
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGTCTGTCTCTTCTTTT
TTTTCTCCGGTCGCATCCCGGGGTGGGTAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGAOCTCCATCCTGGGGGCCATGTGCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGACAACAAGAAGAGGAAGAAGTGAAGAGCTCCGGCCCTGATCCAGGACTGC
ACCCACACCCACCGTCCAGGCATCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAGGTTTTAGGCCAGGCGCCTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTTCAGAGACCAGCCTGGCCAAACATGGTGAACCTTC
GTCTCTATTAATAAATAACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
TCGGGAGGCTGAGCGAGGAGAATCGCTTGAAACCAGGAGGAGGAGGTTCAGTGAGCCGAGA
TCGGCCCACTGCACTCAACCTGGGTGACAGACTCTGTCTCCAAACAAAACAACAACAA
AAGATTTTATTAAAGATAATTTGTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWWLALGQCVLAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKK
EAPPDNKKRKK

FIGURE 26

GAGTCTTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT
 GGCT**ATG**TTTCGTGTCCGATTTCGCCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
 CAGTGTGACCAAGTGCATATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCGCCACAACACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGCGAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAATAAA
 TTTGGGATGAAGGACATGCGCGTGACACTTTCAGCATTCATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGAGCTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCTGGAAGTGCACAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGAC
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCTTTGTGTGTTGACAAAGAACCAGGCGCTGCAAACTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTATTTCCCTCCTGTCTC**TAG**GAATTTGATTCTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTATGATTGAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDDEHSGNDSGSEPSEKRTLREEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFTQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGI PPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAAGCTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAGGAGCAGTATCAGAAAAACCCCTCAACCCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTTTTTTGGAAAGCTAA
 GTCTTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATT
 GAGTAAAGTACGTCCTGGTCAACATGGTGCACGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTCTCTCTGATGTGTGAGATCCGATATGGTGGAGTCACTTTTGACAGAGTCTGTGGC
 CAGCGGCTGCCAACGGTGTCTGTACTCTGAGGACCCCTGGATCTCGCCATGTATCTCTCAG
 CCTCTTCTCCGCCGCCGCCAGCGCCCTGCGTGTAGATCAGACCCTACATTAATATACCATC
 CTGAAGGGTGACAAGAGGGGACCCAGGCCCAATGGGCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCGGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GCGGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCAGCGCGGCAGTTTGTCTGCCCTGCCGTGGCATCTACTTCTTCAGCTCAATGTGC
 ACAGTCTGGAATTACAAGGAGAGCTACGTGCACATATGTCATAACCAGAAAGAGGCTGTCTATC
 CTGATCGCCAGCGCCAGCGAGCGCAGCATCATCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGTCTGGGTGGCGCTCTTCAAGCGCCAGCGCGAGAAGCCATCTACAGCA
 ACGACTTTCACACCTACATCACTTTCAGCGGCCACCTCATCAAGGCCGAGGACGATGAGGGG
 CCTCTGGGGCACCCCTCCCGGTGGAGAGCTCAGGTGCTGGTCCCGTCCCGTCAAGGGCTCAG
 TTGTGACTGCTGTGAAGCAGGAAGGCCAGGGAGTCCCGGGGAGCTGGCATCTGGGGAGA
 CCGTGCTTCTATCTTGCTGCGCATCATCCTCCACGCTATTTCTGCTCTCTCTCTCTCTCT
 TGGACCTATTTTAAAGAGCTTGTCAACCTAAATATTCTAGAACCTTCCAGCCTCGTAGGCC
 AGCAGCTTCTCAAACTTGGAAATGCGATGCGAATCACCGGGGGTTCGTGTTAAATGCAAGATTCT
 GACTCAGCAGGCTATGAGAACCACTGGAGCAACAGGTTCTTAGGACTTTCTCAATATCTTAG
 ATGGGGTCAAGTCTATGAACCACTGGAGCAACAGGTTCTTAGGACTTTCTCAATATCTTAG
 TACTTTCTGAACATTTCTGGAATCTCCCACTTCTAGAATTCTCCCAACATTTTTTTTTCT
 TGAGACAGAGCTTGTCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC
 AACCTCTGCTCCGGGTTCAGCGATTCTTCTGCCCTCAGCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTTGCTAATTTTGTATTTTGTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGTGTGTTTGAATCTTGACTTCAAGTGACCCACCCGCTCGGCCCTCTCAAAAT
 GCTGGGATTCAGTGTGTAGCCACCGTGCTGGCCAAATTCACACATTTCTAAATTTCTCTAT
 CCTCCAGGCTCCCGCTGTATGTTCTTTTACCCCTTCCCGCTTCTCTTGTCTCAGGCC
 TGCAACCACTCAGGACCGTGTATTTATTATTATTAAACACTGAGCACTACTCTGTGCT
 GGTCCCGGGAAGGGTGAGGGGTGACACAGGCCCTGCCCTGCCCTCAGTGACTGGGCCA
 GTCCAGCCAGGCCGGGAGAGATGTGTACATAGGTTTTAAAGCAGCCAGAGCTCATGGGG
 GCTCTGTGTTCTGGGTCTTCAAGTGTGCTGTGCTCCATACCATGCTCCCCAAGGCTGG
 TGGGACGGGTCCTCGGTGGCAGGGGCGAGTATCTCTTCCGTTCTCTATCCACCTCCCCAG
 TGCTCATCGTTACAGCAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCAATTTGGGGGTGAAGTGGCCCGGCAAGAAATGGAACCCACACCA
 TAGCTCTCCCCACAGCTGATACGGCATCTGCGAGAAGACCTGCCCTCTCACTGGGATCCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGGTCAAGTCCCTTCCACCAAGGTCATCT
 GAACTCCGTTTCCCCAGGGCTCCAGCTGCCCTCAGACATGATGTCTGTGCCAGGTGCT
 CTCTGCCCTCTATGCCCTCTCACCAGGCCAGTGGCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGGTGGGACGCTCTGCTCAGAGCCCTCCCTCGGCTGGTGGCTGCTGCTTTAC
 AAACACTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGGAGGACCTCAGGCTTCCGTTTCTTCTCCAGGGTGGGGTGGCTGGT
 GTTCCCTAGGCTTCCAAACCCAGGTGGCTGCCCTTCTCCOCAGAGGAGGCGGCCCTCCGC
 CCATTGGTGCTCATGCAGACTCTGGGGTGGAGTGCCCGGGGGTGATCTCTGTGGTCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACACCCCTGCCGTGATCTGACCTGACCCGCCAGCGCTGCC
 GTCCAGCATGATTAAAGAAATGCTGTCTCTTGGAAAAAAGAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGMPGLPGYMGREGPGQGEQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENATYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCCGCCCTCCCGGGACAGAAGATGTG
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGGCCTGGGGTGCAGG
 GCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGAGCTGCCACCCGACACGGTGGGGCTGTAGCTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCTGCACTCTTGACCTGTCAAC
 AGAACCCAGATCGCCAGCTGCCAGCGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAAGGCTGCATGAAATCACCATGAGACCTTCCGTGGCCTGCCGGCCTG
 CGAGCGCCTCTACTTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACAGC
 TCGACCGCCTCTGGAGCTCAAGCTGCAGGACAACGAGCTGCCGGCCTGCCCGCCTGCGC
 CTGCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTTCAGCCGCTTGCACAACCTCCAGCAGCTGGATGTGTCCGACAACCACTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACAC
 CGCATTTGCCAGCTGCGGCCGAGGACCTGCGCCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTTAAGCTGCAAGGCCTGCTGCGGACCTTCTCGGGCCTCTTCCCGCCCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTGGGCCCTG
 GGTGCGCGAGAGCCAGTGCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACCTGCGCCGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCGCAGCCACC
 ACCACAGCCACAGTGCACACACAGGCGCGTGGTGCGGGAGCCAGCCCTGCTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCAACAGCGCGGCCACTGAGGCCCCAGCCCGCCTCCCA
 CTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCCGTCCACTGCGCTC
 AATGGGGGCACATGCCACCTTGGGGACACGGCACCACTGGGCTGCTTGTGCCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGCTCA
 CGCCGAGGCCACACCGTCCCTGACCTTGGGCATCGAGCCGTTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGTGGTGACGCTGCGACTGCCTGCTCGCTCGCTG
 AGTACACGGTACCCAGCTGCGGCCCAACGCCACTTACTCCGTGTGTGCATGCCCTTGGGG
 CCCGGGCGGGTGCCGAGGGGCGAGGAGCCTGCGGGGAGGCCCATACACCCCCAGCCGTCCA
 CTCCAACCAAGCCCCAGTCAACCAGGCCCGCAGGGCAACCTGCCCTCTCTATTGCGCCCG
 CCTTGGCCCGGTGCTCTTGGCCGCGCTGGCTGCGGTGGGGGCAAGCTACTGTGTGCGGCGG
 GAGCGGGCCATGGCAGCAGCGCTCAGGACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCT
 GGAAGCTGGAGGGAGTGAAGGCTCCCTTGGAGCCAGGCCCAAGGACACAGAGGGCGGTGGAG
 AGGCCCTGCCACGGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGGCTGGCCTC
 CAGTCAACCTCCACGCAAGGCCTACACTAGGCCAGAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTGCGCCAGTGAAGTGGCCAGCCCCCTCCTGCTGCCACACACAGCTAAGTTCTCAGTCC
 CAACCTCGGGATGTGTGCAGACAGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGAGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACCTCCCAAGAC
 CGAGTGCCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCACTGCCCTGGGCACGGCG
 GGCCTGCCATGTGCTGGTAACGCATGCCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCTTGGGGGAGTGAAGGAAGCTCCCGAAAGAGCAGAGGAGACGGGGTAGGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATTCTG
 GGAAGATGTTTTCAAACCTCAGAGACAAGGACTTGGTTTTTGTAAAGCAACAGATGATATG
 AAGGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFEN
 GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
 RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
 GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLHDVSDNQLERVPPVIRGLRGLTRLRLAG
 NTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
 PWVRESHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALS
 SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCP
 GFTGLYCESQMGQTRPSPTPVTPRPPRSLTLGIEPVSPTSRLRVGLQRYLQGSSVQLRSLRL
 TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPGLGPRVPEGEEACGEAHTPPA
 VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAG
 PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPLQSPHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAATAAGTGGTAAATCCTTGAAAAATAC**ATG**AGACTCATCAG
 AAACATTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGTGTGCTCCAGAGCTGCCAG
 AAGAAAGGGGACTGATGACCACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGAGGCACAACGACACTGGATTTATCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA
 TTTTCTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATTAACAGATTAACAGCTGG
 ATCTCAAAACCTTTGGATTCAACAAGGAGTTAAGATATTTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTTGGTATTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCGCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAAATCAGATTTCCGAAAAATTGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTGCAAGACTCTCCCTCATTATGAAGAAGGTAGCCCTGCCCATCTTAAACACAC
 AAAACTTGCACATTTCTTTTACCATGGACAAAAATTTCTGGGTTCTTTTGGGTGATGGAATCA
 AGACTGCAAAAATTTAGTTTAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAGTTTGA
 ATGCAACCAATTTAGTTTAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAGTTTGA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAATTTGTTGGCATACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAATTAATCTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTACAGGTGTTTACATTC
 ACAGGATAAAATCTATTGCTTTTGACCAAAAATGGACATGAAACCTGACAATATCAAAATG
 CCAAAATGCCACACATGCTTTTCCGGAATTTCTCAGAAATTTCAATTTTAAATTTTGGC
 ATAATAATCTTAACAGCAGTGTGTTTAAAGAACTATCCAATCGCTCACTTGAAACCTCT
 CATTTTGAATTCCTATAAAGTGGAGACACTTTCTTAGTAAGTTGCTTTGCTAACACACATC
 CTTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAATTTGCTCA
 TGCCAGAACTCTGGTCAATGAACTGTCTACAAATAAATTTGCTGATTTGCTCTCAG
 GCTCTTCCCAAAAGTATTCAAATCTTGACCTAAATAAACAACAAATCCAACCTGACCTA
 AAGAGACTATTTCACTCTGATGGCTTACGAGAACTAAATATTGCAATTTAATTTTCACTGAT
 CTCCCTGGATGCACTATTCTAGTAGACTTTCACTGTTCTGAACATGAAATGAACTCATCT
 CAGCCATCTCTGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATCGGGGAAGAA
 ATCCATTCGGGTGTACCTGTGAATTAATAAAATTTCACTCAGCTTGAAACATATTCAGAGGTC
 ATGATGTTGGATGGTCAAGATTCATACACCTGTGAATACCTTTAAACCTTAAGGGGAACCTAG
 GTTAAAGAGCTTCATCTCCACGAATTTATCTGCAACACAGCTCTGTTGATTGTCCACCATG
 TGTTATTTATGCTAGTTCTGGGTTGGCTGTGGCTTCTGCTGTCTGGATTTGATCTGGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGTTTAGGAAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCGGATTCACGCAATTTATTTCAATGAAATGAAACATGATTTCT
 TGTGGGTGAAGAAATGAATTTGATCCCAATCTAGAGAAGGAAGATGTTTCTATCTGATTTG
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCATTGA
 GAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCGAGATGAGTGGTGCCATT
 ATGAATTTACTTTTGGCCACCACAATCTCTTCCATGAAAATTTGATCATATAATTTTATC
 TTACTTGAACCAATTCATTTCTATTGCAATTTCCACAGGATATCAATACTGAAAGCTCTCTCT
 GGAAAAAAGCACTATTTGGAATGGCCCAAGGATAGGCTAAATGTGGGCTTTTCTGGGCAA
 ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACAGAGAAATGTATGAATCGCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTTGCT
ATAAATCCCAAGCTCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
 CAACTTTATGATGGCAATTTGCAATATTTTAAATAAATAAGTATTTTCCCTTCTATGATA
 CAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACCTTCAAGTTTATAAAG
 GCTTTATGAAAAAAGGTGTTTCAATCCAGGATTTGTTATAATCATGAAATGTGGCCAGGTGC
 AGTGGCTCAGCTTTGTAATCCAGCACTATGGGAGGCCAAGTGGGTGAGCCACGAGGTCGA
 GAGTGAAGACCATCTTGCCCAACATGGTGAACCCCTGTCTACTAAAAATACAAAAATTA
 GCTGGGCGTGTAGTGGTCAGCCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGGATCG
 CTTGAAACCGGAGGTGGCAGTTGCACTGAGCTGAGATCGAGCCCTGACTCCAGCTGGTGT
 GACAGAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCATGGCCCAATAAAGTTCTAATTCATAAATTTATAGTACATTAATTAATATAATTA
 CATGCCCAATAAAGAAATAGGTAGCTGTATATTTCTTGGTATGAAAAACATATTAATAT
 GTTATAAATATAGGTTGGTGCAAACTAATTTGGTTTTTGGCATTGAAATGGCATGGA
 ATAAAGGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTTGGGTCTGGGAGGTTGA
 TTAACAGGAGCATTTGATTCTATGTTGTGATTTCTATAATGTTTGAATGTTTGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCTT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCWPETVVNMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMAIRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVGVWSDSYTCYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMVLGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTTEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKISSENI
VSFIEKSYKISIFVLPSPNFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKGLFWANLRAAINVNLATREMYELQTFTELNEESRGSTISLM
RTDCL

GGGGGCTTCTTGGGCTTGGCTGCTTGGAAACACCTTGCCCTCCAAGGACCGCGCTCGGAGGGGTGCGCGGGAAAGG
GAGGGAAGAAAGGAAGGCGGGGCGCGGCCCTCCGCGCCGCGCCCGCGCTCTGCGCGCCCTTGCGCCCGCGGC
CCAGCCAGCCAGCCAGCCCGCGCGCGCGTGCACGCGAGCGAGCGCGCGCTCCGCGCGCAAGCGCGCGCTCT
CTGCTGTGCTCTGCGCCCTTGCCGCGCGCGAGCTTCTGCGCGCGAGCGCGCGCGCGCGCGCGCGCTGACCTGTA
CCTGCGCTTGGGCGGGGGCGGAGGCGATGTCGCGCGGGGACCGCTACCCAGCGCTGGCGCTGGCTGCT
CTGGCAGTGCCTTGCCTGGGGGTGGAGCGCGAGGCGCGAGCTCGAGGACCTGATTATTGCGCGGAGGAGAT
CTGGAGCGGGAGCCCTACTACGCGCGCGGAGCCGAGCTCGAGACCTTCTGCGCGCTTGGCTGGCGGGG
CCGGGAGGAGATGGGAGCGCGCGCGAGGAGCCGAGCGCGCCCAAGAGGGCGCAAGCGCGCAAGAGCTCCC
AAGAGGGAGAGATCGCTCGCGCGCGCTTCCACAGGTAAACACGACAAAAGGTTATGAGAACAGAG
CTCTGAGAGGCTGCCAAGCATGATCACAGTGTCCGTGTGCGCGCTGAGAGTGTGAGAGAGATTGGCCACTC
CATCGAGGAGGACTACATCATTCAGCGGGGCTTAATGAAGATGATTTATGAGCGAGCGTGGTGGCGGGGAG
AAATGAACCTCCAGCAGTGAATGAAGTGGATGCTGCGCGCTGACCAAGTCTGCTGTGATAATGGAGCATCTGCAT
GAGCTTCCCTTGGCTGAGTGACTGGGTGAGTACCTTATAGGTCTGTCGAGCATCGAGCCACATGCTGGGT
ACTGTTAAGAAATGGATCTGGAGACATGATATTTGAGGAAACAGCTGAGAGAGATCCGCTTCTCAATGAGCT
ACCCGTCGCCATGGTGGCGCGCTACATCGCGATAAACCCCTCAGTCTGTTGATAATGGAGCATCTGCATGA
GATGAGATCTGGGCTGCCCATCGGCATCGCAGATCTATAATATTATTCAGCGCGGAGACGATGACCACT
GATGACCTGGATTTTAAAGCAACCAATTAAGGAATAAGCGCGATGTGTAAGAGTTGTGAATGAATGTGTC
CATATACACAGAAATTTACAACATTTGAAAAGAGCCACAGGCGCTGATGTCTGTGAGATCTCAGATC
ACCTCGGGGAGCATGAAGTCGCTGAGCCGAGTTCATCATCTCGCGGGGCGCCAGCGCATGAGTCTGCGC
CGGGAGCTGCTGTGCTGCTGTGTCAGTTCCTGCTTCTCAGGATGACTGGCTCGGAATGGCGCATCTGCTGCGC
GTGGAGGAGAGCCGGATTCAGTCTCCCTGCTTCAACCCGATGGGCTAGGAGAGCGCTACGAAAGGCGT
CGGAGCTGGGGGCTGTCTCGCTGGGACGCTGGAGCCACGATGGAATGACATCAACACAACTTTCTGATTTA
AACACGCTGCTCTGGGAGGACAGAGATCGACGAATGTCCCGAAGAGTTCCCAATCATATATTGCAATTC
TGATGTGTTCTGTCGGAAGAAATGCACGCTGGCTGCCGAGCAGGACGATCATGCTGGATGGGAAAAATC
CTTTTGTGCTGGCGGCAACCTCGAGGGCGGCGAGCTGGTGGTGGCGATCCCTACGACCTGGTGGGTCCCC
TGGAAGACGCGAAGACACACCCCGCCCGGATGACCCAGCTGTTCCGCTGGCTGGCTCTCTATGCTCCAC
ACCCGCGCTCATGACAGACGCCCGGAGGAGGTTGCCACGAGGAGCTTCGAGAAGGAGGGGACGCTGTA
ATGGGGCTCTGGGCGCTGATCTGCTGGAAGTCTGGAACGATTTAGCTACCTTCATACAACCTGTTGGAAC
TCATCTACGTGGGACGATGATAAATACCACTGAGAGCGAGCTGCCGAGGATGGGAGATACCGGAACTG
TCTGATCTGTTCATGAGAGGCTTATCTGTGGCATTAAGGCTTTGTCGAGAGATTCCGATGGAAGAGGAATCC
CAAACGCCATTATCTCGTAGAGGCTATTAACATGACATCGAACAGCCAGCATGGGATTACTGGCGCTC
CTGAAACCTTGGAGAGATTGTGTTGCTGACGAAAGCGGAGGTTTTCATGTCATCCACAGAGACTTATGGTTGT
CTATGACTGTGGGGCGACAAGTGTGACTTCACATTCGACAAACCAACATGGCGAGATCCGAGAGATCATGG
AGAAGTTTGGGAGAGCCCGCTCAGCCTTGCACGAGGCGGCTGAAGCTCGGGGCGGAGAGAGACGACAGCT
GGCTGACCTCTCGGCGCTTGAGACTCTGGGACCTGCAAAATTAACCAACCTGTGTAGTAGCTCCATG
TGACATCAGCTACTGTTTCTCTGTAATTCAGAGATGCTGGAGAGAGGGTGCAATTTGAGGCGAGGTCC
CAAAAGGGAAGCTGATGGGAGTGAAGCACTGTTTCTTTCTTTCTTCTTCCATTTCTCAGAGTTTGTGGGACGAAGCA
CGAGAGCAAAAGCTGATGGGAGTGAAGCACTCAGCAAGCCACCTGGGAATCAGAGAGAGAGGAGAGGAGGG
GAGCGCTGCTCGCTTCCAGGCTCTGGCTCATGATAAAGAGATTCTGTGCTTCCCTGTTTGGCTGGCAGAGG
GTCCCTCGATTTGTGCAATTTGCACAGCTAAATTCAGAGATTTCCCGAGCTGGGCTGCTCCAAATGTATACCA
TTTGAGATGCTCCGAGCGCTCTAAGAGAAATCCACCTCTCTGCGCCTGGAGATTCGAGCTGACTACAAATAA
ATTCTGTGTTCTTTGACATAAGCTGATGCCAAGTGCACATCAGTGAAGCTTGAATGTGTTTGTAGTCTCT
TTTCAACAAAGGGGTGTGTTCAAGAAAGGAGAGAGGCTGAGAGTCTCAGAGTTTGTGGGACGAAGCA
TGGAGCTTCTGACAAATTTGGGTCATATAACACGCCAAAGTCCCTGCTGATCCATGCTGCCCTTGTGAGT
CCGCAAGTGGAGAGGACGAGAGTGGCGCTCTGTAAGGGGCGAAATTAAGCTGAGATTTGCCCTTGTATC
CTGCTAGGACTGGAAGAGCGAGAGTGGGTGGCTTGAGGCTCTCTGCTTGAAGATTTGCCCTTGTGCT
GAATTGAGTGTCTGGGTTGGCTCATATCAGCTGGGAGTTATTTTGATATGAGATTCGAGATCTCCA
GATTAGGCTAATGTAATGAACCTTTAGATATTCTGTGGAGCATCAGTTTGGGAGAAATTTGAATTTAT
CTTCAAGAAAGAAATGTATGCTCACTTTTGTAAITGTGCTGCTCATGTGACCTGGGAAATTTGAAAATAA
AATAAGACAAATGGTAAGACCTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

GGGGGCTTCTTGGGCTGGCTGCTTGGAAACACTGCCCCCAAGSACCGGCTCTGGAGGGGCTCGCGCGGAAAG
 GAGGAGAGGAGGAGGAGGGGGGGCGCGGCCCTCTGCGCCCGCCCGCGCGCTCTGCGCGCCCTCTGCGCCCGCG
 CACCGCCAGCCAGCGCCCGCGCGCGGTACACGCGAGCAGCAGCGCGCGCTCCGCGCCCAAGCGCGCGCT
 CTGCTGTGCCCTGCGCCCTTCCGCCCGCGAGTCTTGCGCCGCGACGCTCCCGGGCGCCCGCGGTGACCTGTGA
 CCTCTGCTTGGGCGGGGCGAGCAGCACTGTCGCGCGGGAGCGCTACCCAGCGCTGGCGTGGTGTCT
 CTGGCAGTGCACCTTGGCGGGGTGGAGCGCCAGGCGCAGCCTCTGAGAGCCTGATTATTGGGCGAGGAT
 CTGGAGCGGGAGGAGCTTACGTACGCGCCGAGGAGCCAGACTCGAGACTTCTCTCGCGCTGTGCGGGG
 CGGGGAGGAGTGGGAGCGCGCCGCGAGGAGCCAGGCGCCCAAGAGGGCGCCAGAGCGGAAAGCTCC
 AAGAGGAGGAGTGGCTCGGAGCGCTCCACAGGTGAACACAGCAAAAAAGTTTATGAGAACAGAG
 CTCTGAGAAGCTGCCAAGATGATCAGCTGTCTGCGCCGTGAAGATGTGAGAGAGATGTGCCACTT
 TTGGTGTGAAACCTTAAATACAGACTTCAGCTCCATGTCCAGCTGAAGCGATTTGGCTGGGGG
 CTGAGGAGAGCTCACATCAGCGGGGCACTTAATGAAATGATTTTATGAGAGCGGTGTGTGCGGGAGG
 AATGACCTTCAGCACTGGAATGAAGGTGATCTGCGGCGTACGACAGTCACTGGTGTATCATCAAGGA
 GSAACCTCCCTCTGCTGAGTGACTGGTGTACATCTTAAGTGTATGTGAGCAATGACGCCACACGTGGGTCT
 ACTGTTAAGAAATGATCTGGAGACTGATTTTGGAGGAAACAGTGAAGAGATTCCTGTCTCAATGAGCT
 ACCGCTGCCATGSGTGCGCGCTACATCCGATCAACCTCAGTCTGTTTGAATTTGGAGAGCTTGCAATGA
 GATGAGAGATCTGGGCTGCCATCGGCAGATCTAATAGTAATGCCAGCTTGATGAAGTTTGTAATGAATGTGTCC
 GTATGCTGGATTTTAAAGCAACTTAAAGTAATGCCAGCTTGAAGTGTATGCTGGAGATCAGATC
 CATATTCACAGGAATTTACAACTATGAAAAAGCCAGCCGAGCTGAACTGTATGCTGGAGATCAGATC
 ACTCTGGGAGCATGAAGTGTGCGTGAGCCGAGTTTCACTACATCGCGGGGGCCCCGCGCATGAGTGTGTGGG
 CGGGAGCTGCTGCTGTCTGTGTCGAGTTGTGTGTTCAGGATATCTGGCCGGAATGGCGCATGCTCCACT
 GGTGGAGGAGAGCGGATTCAGCTCTCCCTCCCTCAACCCGATGGCTGCTGAGAGAGGCTACGAGGGGGCT
 CGAGCTGGGAGGCTGTGCTCTGGGAGCTGCGACCATGAGTGAATGACATCAACAACTTTCTGATTTA
 CCAAGCTGGCTCTGGGAGGAGAGATCGACAGATCTGCCAGAAAGTCCCAATCACTATTGTCAATCCC
 TGAGTGGTCTTCTGTGCGAAAGATGCACCGTGGCTGCCGAGACGAGAGCATATGCTCGGTGAGAAAAATC
 CTTTTGTCTGGGCGGCAACTCGAGGGCGCGAGCTGGTGGTGGAGTATCCCTACGACTGTGTGGCTCCCC
 TGGAAAGCAGGAGAACACACCCGCCACCCGATGACCACTGTCCGCTGGCTGCTACTCTTGCTCCAC
 ACACCGCTCTATGCAGACAGCGCCGGAGGGGTTGGCCACGGAGACTTCAGAGAGGAGGAGGCATGTCA
 ATGGGGCTCTGCGGCACGCTGCTGTGAAGTCTGGAACGATTTCACTACTTCATCAAACTGCTTGAAGCT
 TCCATTCAGTGGGCTGTGATTAATACCACTGAGAGAGAGCTGCCCGAGGATGGGAGAAATACCGGAATC
 TCTGATCTTTGTTCATGGAGAGGTTCATCTGTCGAGATTAAGAGCTTGTGAGAGATTCATGTGAAAGAAATCC
 CAAACGCCATTTCTCGTAGAGGATCACTGACATGACATCGAACGCCAAGATGGGGATATGCGGCGAATC
 CTGAACCTCTGGAGATGATGTTGTCACAGAAAGCGGAAGTTTCACTGATCCACAAAGACTGTATGTTGTG
 CTATCACTATGGGGCCACAGGTGTGACTTCACTATGCAAAACCACTGATGCCAGGATCCGAGAGATGCG
 AGAGTTTGGGAGCAGCCGTCGACCTTGCCAGCGCGGCGCTGAAGCTCGGGGGCGGAAGACGACAGCT
 GGGTGAACCTCTGGGCGCTTGAGACTCTGCTGGGACCTGCAAAATTAACCACTGTTGATGAGTCCATAG
 TGGACTCACTCACTGTTCTTCTCTGTAATTAAGAGATGCTCGGAAGAGAGGTTGATTTGAGGAGGCTCC
 CAAGAGGAAAGCTGGAGCTGAGGCTGAGGCTTTCTTTCTTTCTGTTCCATTTCAAAATCTTGGACAGGCA
 CGAGAGAAAAGCTGATGGGAGTGAAGAACTCAGCAAGCCAACTGGGAATCAGAGAGAGAGGAGGAGGAGG
 GAGGCTGTGCGTTGAGGCTCTGGCTCGATAGAAAGGATTTGTTGCTTCCCTGTTTGGTGGCGACGAGG
 TTCCAGCTGCTGATTTGCAATTTGCAAGCTAAATTCAGCAATTTCCCAAGCTGGGCTGCTCCAAATGTTACCA
 TTGAGATGCTCCAGCGCTCTAAGAGAAATCCACCTCTCTGGCGCTGGAGATTCAGAGCTGTACAAATAA
 ATTCTGTGTTCTTTGCAATAGCGTCACTGCCAGTGCATCTCAGTCAAGAGTTTGTGGGCGACCAAGCA
 TGGAGCTTCTGCAAAATCTGGGTCGATAAAGACCCCAAGTCCCTGCTGATTCAGTAGATCTTCTTTTAC
 CCCCAGTGGGAGGACGAGGCTGCGACCTTCTGAAGGGCCAGAAATTTAGCTCTGATTTGCTTCTTTTAC
 CTGCTAGGACTGAAGAGGCGAGAGTGGGTTGGCTTGAAGCCCTCTCTGCTGAGSTATTGCCCTGTGTG
 GAATTGAGCTCACTGGTGGTGGCTCATCAGCTGGAGGTTATTTGATGTAGATGCAAGTGCAGATCTTCCA
 GATTAGGTAATGTAATGAAACCTCTTAGATATCTGTGAGACATGATTTGGGAGAAATTTGTAATTAAT
 CTTCGACGAAAAATGATGTCTCACTTTTGTAAATGTTGCTGCTCATGTACCTGGGAAAAATGAAAAAA
 AATAAAGCAATTTGTAAGACCCCTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPLP
AGPGEEWERRPQEP RP PKRATKPKKAPKREKSAPEPPP PGKHSNKKVMRTKSSEKAANDDHS
VVRAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLDPFNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNP DGYEKAYEGG
SELGGWSLGRWTHDGI DINNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAMMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTEHTPTPDDHVFRWLAYS YAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAAISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVS L PARR
LKLGRKRRQRG

FIGURE 37

CTAAGAGGACAAGATGAGGCCCGGCTCTCATTCTCCTAGCCCTTCTGTCTCTCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATCTGGGACCTCCAAATCCAGCCCGGCTTCAGCTCTTCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTCTGTGTCCAGTTGTT
 TTCCAAATTTACCCGGCTCCGCTGGATGACCGTGGGAGCTGCCAGTGCTGTGTTCCCTGCCAGACACCACTTTTC
 CCGTGGACAGACTGGAACGCTTGGAAATCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA
 GTAGGGAATATGTCCAAATTAATTAGTCTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATGACATCAT
 GGAAGAGGATACCAATTTCTTACACGTGAGGAGGTTTGGTGGAGCTCAGAAATGTTGACCAAGCTGGAGGTGGAGATAGAAAT
 ATGACTCTCTGTAGGAGAGCTTGGAGCACTAGACAAAACARTGTCTTGCATTCCGCCGAGAATCTGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTTAAAGATCAAACACCCCTGTCTGCCACCTCTCCCACTC
 CAGGAGCTGTGTCTCATGTGTGTGTGGTGAACATCAGCAACCCGCTGTGTGTTCAAGTCAACTGGAGAGGTTT
 TCTTATCTATATGGTGCTTGGGTAGGGATTACTCTCCCGAGCTCCAAACAAAGGACTCTATTGGGTGGCGCC
 ATTTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACACAAACACATGTACCTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAAATG
 GATTGTGGGTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCAACGCCTTCATGGTATGGGGTTCT
 GTATGCCACCGTACTATGAACACCAAGCAAGAGATTTTACTATTATGACACAAACACAGGGAAGAGG
 GCAACTAGACATTGTAAATGCATAAGATGCAGGAAAAGTGCAGAGCATTAACTATAACCCCTTTGACCAAGAA
 CTTTATGTCTATAACGATGTTTACCTTCTGAATATGATCTTTCTGTCTTGCAGAACCCAGTAAAGCTGTTTA
 GAGTTAGGGTGAAGAGAAAATGTTTGTGAAAAATAGTCTTCTCCACTTACTAGATATCTGCAGGGGTGT
 CTAAGAGTGTGTTTCTTGGGAATCATCTGCTCTTCAGGCGCAATTTTGCATTAAGTCTGTCTAGGGTGGGA
 TTGTTCAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCTTAAATTA
 GCAATTAAGGAACCTTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAATATTGCCCAATGACTAGTC
 CTCATCCATGTAGCACCCTAATTTCTTCCATGCTGGGAAGAACTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAGCTCTCGAGGGACCAATCTCCAACCTTTTTTCCCTCACTAGCACCTGGAAATGATGCTTTGATATGTTG
 CAGATAAGTAATTTGGCATGCTTATATATTTCTACATCTGTAAGTGCTGAGTTTATGAGAGAGGGCTTTTT
 ATGCATTAATTTGTACATGGCAAAATAATCCGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTC
 ATTGTCCACCTTACTAAAGTTCAGTAGAATCTTCTACCTCATAACTTCTTCCAAAGGCAGCTCAGAAGATTAG
 AACCACTACTAATACCAATTCACCCGCCACCAACCCCTTCACTGCTACTTTAAAAAATAATAGTTT
 CTATGGCACTGTCTAAGATTAGAAAAATTAATTTCTTTAATTTCAATTATGAGCTTTTATTTACATGACTCTA
 AGACTATAAGAAAACTGTAGTGGCAGTGACAACTGCTAGCATTTATGTTATCTAATAAGACCTTGAGCATA
 TGTGCAACTTATGAGTGTATCAGTGTGTTCCATGTAAATTTTGCCCTTTGTTTAAAGCCTGGAACCTGTAAAGAAAT
 GAAAAATTAATTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGTGGGTATGTGATGTGCTCTTGAATGACTTTATCATCTAGTCTTTGCTATATTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAAGTAT
 TAAAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

MRPGLSFLLLALLFFLGLQAAGDLGDVGPPIPSPGFSFPFVDDSSSSSSSSSSSSSSSSSSRLGS
GGSVSQFLSFNFTGVSDDRGTCQCSVSLPDTTFPVDRLVERLEFTHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLTDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGlyWVAPLNTDGRLLLEYRYLNTLD
DLLLYINARELRITYGQSGTAVYNNMNMVNMNTGNIARVNLTTNTIAVTQTLNPAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTAETGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLVYATRMTNTRTEEIIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTTGTGACGTTTGTGGAGATGGGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCAATGTTTGTGTGGGAAGTGCCCGTGTTTGTCTATGCCGATGCTGTCCATAGTGAAAC
 TACCTCAGCTGTAATAGATTGATCTATGCACTTTTCTTGGTGTGTGGAGTATGTGTAGCTTG
 TGTAAATGTTGTATACCAAGAAATGGAAGAACACTGAATAAGATTCTCTGGATTTTGTGAGAAATG
 AGAAAGGTGTGTGCTCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GCTTTGGCTATGTTCTTCTCTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA
 TTATTGGGCATTCTCTCATTCCAGAAGGAACTTTACAACGTGTGTGGTTTATGTAGGCCATG
 CGAGGTGCCCTTTGTTTTCATCTCATACAACCTAGTCTTACTTATTGATTTTGACATTTCTATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTAATCTGCTGCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTGAGAAAACAGGCGTTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCCTCTGTAATGTCTATACTGCCAAAATCCAAGAATCACAACCAAGATCTGGTT
 GTTACAGCTCTTCAGTAATTACAGTCTACACAATGTATTGACATGGTCAGCTATGACCAAT
 GAACCAAGAAACAAATGCAACCAAGCTCTACTAAGCATAATTGGCTACAATACAACCAAGCAC
 TGTCCCAAAGGAAGGGGAGTGCAGTCCAGTGGTGGCAGTCTCAAGGAATATAGGACTAATTCT
 TCTTTTGTGTGTGTATTTTATTCAGCATCCGTACTTCAAACAATAGTCAAGTTGATTAATAAA
 CTGACTCTTCAAGATGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGTAGGAATC
 ACTGGAGGATGGGAGCAGTGTTCACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATTCTCTTCTTTCATCTTCTGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC
 AACTGGTCCAGGATGAACCCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTCCAGTTGGATTGGCATCGTGTGTTATGTTGGACAGCTCGTGGCACCATTGTTCT
 TTACAAATCGTGATTTTGACTGAGTGAAGCTCTAGCATGAAAGTCCCACCTTTGATTATTGCT
 TTATTGAAAACAGATTTCCTCACTTTTGTAAAGTTGTGTATGTTTTGCTTCCATGTAAAC
 GTTCCAGTGTCTCGCATGAATTAGATTTTACTGCTTGTGCTTTTGTATTCTTCTTACCAG
 TGTCTTGTATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTATGTAATGTGTGATGAGT
 TAGTAAAGATGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAATGTTGTTGACTATTTTAAAATTATATAGACCTTAAGCTGTTTTAGCAAGCATTTAAA
 CCAATGTTATGGCTGCCCTTTTGAATTTTGTATGTGTGGCTGGCAGGATAGTGCAAAAGAAC
 ATGGTTTATTTTAAAATTTATAAACAAAGTCACTTAAATGCCAGTTGTCTGAAAATCTTTATA
 AGGTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTAGTGGCAATAGTGTAGG
 TTTATGGATGGAGGTGTGCGTACTAAATTAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGGCAAAGGTGAAGCTGTTTGGTTGTTTAAACTCATGAAGTATGGGTTCAGT
 GGAATATTTGGAACTCTGAAGGATTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTTAGTTTGGGCCAGCAGCGTAGCTCACCCCTT
 GGTAATGCCAGCATTGGGAGCTTAAGTGGGTAGATTACTTGAGCCCAAGGAATTGAGACCA
 GCTTGGCAGATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCTCTGGGTC
 CAGCAGCTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCAAGTGAAGCAATCA
 CGTCACTGCACCTTCTAGCTGGCAGAGATTAAGCCAAAAAATATATATATGAAATCAAGG
 AGGCAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGCTATTAT
 ATAAAACTAGTCCAGTTCTCTCATTAAAAAATGAAGACACTGAAATACAGACTTAAATTA
 GCTCAGATGATTAATGGAATTTCAAGTTGGCCAAATAATAGCATCTCTCTGACATTTTAA
 AAATAATTTCTATTCAAATACATGCATATTTGATTTACACCTCATAGCTGTGATTAATTAATG
 GATGTGGATTGCTGTGTCAGCATACCCATAAACAGGTCAGAGAAGATGATGGAATGTTTT
 AGAATAAATCTCTGTTATAGTATATACACAGTTCAAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATTGAAATATATAGATTATTGAACCTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTAGTATTGATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTTCAACAT
 TCTTTTAAAAATTTTATATGTGAATGGAATATAACATTCAGCTTAAATCCCAACAC
 TTATTCTGTGTGTAGACATTGTATCCACAATTTGAATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSWIGI
VLYVWTLVAPLVLNDRFD

FIGURE 42

GCGAGAAAGAAGCTGCTCCATCTTGCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAACTAGATTGATCTA
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACCTGAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCCTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTGNTATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTNTTGGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATGCAATTATTATG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCACTGTAACCTAGATTGATCTATGCACTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGCTATGTTCTATCTTCTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACITTTTCCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTTCATCCTCATACAACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTCAGAAAACAAGGC
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGGCGCAGGAGCGAGTCGGTTTGCCTGCGATTGAGCTCGGGTTCGCGCCGGCGCGGCTCTCCAAT
GGCAAAATGTGTGTGGCTGGAGGCGAGCGGAGGCTTTCGGCAAAAGGAGTGCAGTGTTCGACAGCCGGGGCGAG
TCTGTGAAAAGCAGATAAAAGAAAACATTATTAACTGTGATTACGAGGAGCGCCCGCGGGGCTGTGCG
ACTCCGCGCGGAAACATTTGGCTCCCTCAGCTCCGAGAGGAGGAGAAAGAAAGCGGAAAGGAGGACGATTAC
GCTTGTTCAGCCAAATGGACCTGATCGATGGCCCTCCTGAATTTATCAGATATTTGATTATTAGCGATCC
CCCTGGTTTGTGTGTACGCACACACAGCTGCACACAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCAGCTCC
TGGGCGAATCCACATCTGTTTCACTCTCCGCGGAGGCGAGCAGGAGCGAGAGTGTGCGAATCTGCGAGTG
AAGAGGACCGAGGGAAGAAAACAAGGCCACAGACGCAACTTGAGACTCCCGCATCCAAAAGAAAGCAGCAGAT
CAGCAAAAAAAGAAAGTGGGCCCCCGAGGCTCGTGCTGTGCTTCTGCTCCGCAACTGTCTTCCCTCGTGGG
TGAAGCTCGGGCTTCTGTGCGACACCCGCTGAAAGGAGGTTTCAGAGGAGCCGAGGAACATCCGCCCA
ACATCATCTGTTGCTGACGGAGACCCAGGATGTGAGGCTGGTTCCATGCAGGTGATGAACAAGACCCGGCGC
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCCTCGTGACACACCCATGTGCTGCCCTCAGCTCCTTC
CATCCTCACTGGCAAGTACGTCACACACCAACACCTACACACAAATGAGAACTGCTCCTCGCCCTCCTGCG
AGGCACAGCAGAGAGCCGACCTTTGCCGTGTAACCTCAATAGCACTGGCTACCGGACAGCTTTCTTGGGAAG
TATCTTAATGAATACACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTGCGGACTCCTTAAAACTCCCG
CTTTTATAACTACAGCTGTGTGCGAACGGGTGAAAGAGAAGCAGGCTCCGACTACTCAAGGATTACCTCA
CAGACCTCATCAACCAATGACAGCGCTGAGCTTCTTCGCACTCCAAAGAGATGTACCCGCAACAGGCCGCTCTC
ATGGTCATCGACCATGCGAGCCCCCGGCCCTGAGGATTCAGCCCCACAATATTACGCGCTTCTCCAAAAGC
ATCTCAGCAGCATCAGCCGAGCTACAACTACGCGCCCAACCCGAGCAAACTGATCATGCGCTACACGGGGC
CCATGAGGCCCATCCACATGAATTCACCAACTGCTCCAGCGGAGCGCTGCGACATCCCTCATGTCTGGTGGAC
GACTCTTATGAGACGATTTACAACTGCTGGTTGAGACGGGCGAGCTGGACACACACATCATGATATACACCGC
CGACACGGTTGACCATCGGCGCACTTTGGCTGTGAAAGGGAATCCATGCCATATGATTGACATCAGGG
TCCGCTTCTACGTGAGGGGCCCCAACGTTGGAAGCCGCTGTCTGAATCCCACTCTGCTCAACTCAAGCTGT
GCCGCCACTCTGGACATTCGAGGCTTGGACATACCTGCGGATATGGACGGGAAATCCATCCTAAGCTGT
GGACACGGAGCGGCGGCTGATCGGTTTCACTTGAAAAGAGATGAGGGTCTGGCGGGAATCCTTCTTGGTGG
ACAGAGGCACGCTGCTACACAAGAGAGACAATGACAAGTGGAGCGCCAGGAGGAGAACTTCTGCCCAAGTAC
CAGGCTGTGAAGGACTGTGTGAGCTGTGAGTACCAAGACGCGGTGTGAGGAGCTGGGACAGAAAGTGGCAGTG
TGTGGAGAGCCGACGCGGGAAGCTGAAGCTGCATAAGTGCAAGGCCCATGCGCTGGGCGGACAGAGGCC
TCTCMACTCTGTGCCAAGTACTACGGGCGAGGCGAGGCTGCACTGTGACAGCGGGGACTCAAGCT
AGCCTTGCCGGGACCGGAAAACCTCTCAAGAAGAAGTACAAGGCCACATATGTCCGCACTGCTCCACTCG
CTCAGTGGCCATCGAGCTGACCGGAGGCTGTACACGCTAGGCTGGGTGATGCGGCCAGGCCCGGAACTCA
CCAAGCGGCACTGGCCAGGCGCCCTGAGGACCAAGATGACAAGGATGGTGGGAACTTCACTGGCACTGAGGC
CTTCCGCACTACTCAGCGCCAAACCCATTAAAGTGACACATCGGTGCTACATCTAGAGAAGCAGACAGTCCA
GTGTGACCTGGACCTGTACAAGCTCCCTGAGGCTGGAAAGCCACAGCTGCACATGCACACAGATTTGAAA
CCCTGCAGAAACAAATTAAGAACCTGAGGGAAGTCCGAGGTCACTGAAGAAAAGCGGCGAGAAATGTGAC
TGTCACAAAATCAGCTACCCACCCGACACAAAGGCCGCTCAAGCACAGAGGCTCAGTCTGCATCCTTTAG
AAGGCGCTGCAAGAGAAGGACAGGTGTGGCTGTTCGGGAGCAGAAAGCGCAAGAAGAACTCCGCAAGCTGC
TCAAGCGCCTGCAAGAACACGACACGTGAGCTGCGAGCCTCAGGCGCTCAGCTGCTTCAACCCAGACACGACTGG
CAGACGGCGCTTTCTGGACATCTGGGGCTTTCTGTGCTGCACCGCCACCAATACACGACTCTGTCAT
GAGGACCATCAATGAGACTCAAAATTCCTCTCTGTGAATTTGCAACTGGCTCTCTAGATCTTTGATCTCA
ACACAGACCCCTACGAGCTGATGAATGCAGTGAACACATGGACAGGATGTCCTCAACAGCTACACGTCAG
CTCATGTGAGCTGAGGAGCTGCAAGGTTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACTCTGATGGAG
AAGCTATTGACAAATACAGGCACTTTGAGCTGAAAGTGGCCAGAAATGAAGAGACCTTTCTTCAAACTCAGTGG
GACAACTTGGGAAGGCTGGGAAGGTGAAGAAACAACAGAGGTGGACCTCCAAAACATAGAGGCATCACTGA
CTGCACAGGCAATGAAAACATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCTGAGAAAG
AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACCCAGAGGACAGAGATTAATCTCAGAAAGTCC
ATTTTTCGCTTGTGCTTTTGGATTATACCTCACCAGCTGCACAAATGCAATTTTCGTATCAAAAGTCC
ACCACTAACCTCCCCAGAAGCTCACAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTCTTGGAAATTTTC
TCCGAGGGGCAAGTCAATGGAATTTTAAATCATAGAGGAAAGCAGTCTGTTCTTAAATCCTTTATTCTT
TTGGTTTGTACAAAAGAGGAACATAAGAGCAGGACAGAGGCAACGTTGGAGGGCTGAAAACAGTGCAGAGAG
TTTGAACATGAGTACGTAGCAACAAAAGAGATGACATTTACCTAGCATATAACCTGGTTGCTCTGAAGAAA
CTGCCTTCAATGTATATATGTGACTATTTACATGTAATCAACATGGGAATTTTAGGGGAACCTAATAAGAAAT
CCCAATTTTCAGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAGAAAA

FIGURE 47

MGFPISVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMPHPRPVLMMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHHRDNDKVDAQEEN
FLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKLKHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDVKVLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

09090430716

09090430716

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCACTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA
 CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGTGCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGAGAGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCC
 ATGGCCTGCACCTCCTGCAGTGCACTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC
 TCCAGGCCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCVAGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRVRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSAAATLSPGAS
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FIGURE 52

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCGGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTTGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTAAAAA**ACT**TAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

T0447-240462

FIGURE 54

CCCGGGAACGTGTTCTCCTGGCTGCCGCACCCGAACAGCCTGTCTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCCTGGTGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACATAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACCTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

CTGCTGCATCCGGGTGTCCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGAG
TGAGGCGGGCCGGCGCGGCGCACACCGGCTCCGGAACCATGCACGACGGGCTGGACTG
ACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAAGCTGTATTATATCCACCATTGAAAGATTTCAACCACTCATACCATTGCGT
GTGGTGTTATAGCAACCATAGCCTTCTTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAACAGGTGCTCGCATTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCCTTCATCTTT
TTTGGAGGGCTGTTTATTAGTTTGGCCGCACTGAAGACTATGGCAGTAGCAACATCTGAT
TCCCAACGACACAAACAGCCCTGCATGGGTTTGTTTGTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAAATCTATTGTGGTATGCACCTTGATTAACCT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTATCATGGTATAATT
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCTATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTATTCAATGTGGT
CTCTCTGTGTGCAAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAAAATATCCGTGG
TCAAAATTTCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATTTCTGTGAACATGTAAT
GTAACCTGGCTTTTGGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCAT
CCAAGTCCAGGAAGAGTGTGACTCAGCATTGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCGCCACTG

57/330

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

399033-11401

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATAACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCACCATGAAAGATTTNAACCACTCATAACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCCTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTCCAGAATGCC

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTACAGGCTGGTGGATTATNATAGATGACGCTGTTATTT
ATCCCAACCATGAAAGATTNAAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCGATATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTGGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTATGTGGATTNTTTTGGAGGTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGCGCGG
CGNGACACCGGGTTCGGGAACCATTCACGACGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGT**ATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGCGCGTCC
TCTGCAAACTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCGCCCAAGCGCCCTGGTAACGTACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
TTTTTTCAGCCAAACCAAGTCCGCGAGAAGCTGGATGTGGTGGAATTTGGCAGTGGCTTTGGGG
GCCTGGCTCAGCTGCZAATTAGCTAAAGCTGGCAAGCGAGTCCCTGGTCTGGAAACAACAT
ACCAAGGCGAGGGGGCTGCTGTACATACCTTTGGAAAGAATGGCCCTTGAATTTGACACAGGAAT
CCATTACATTTGGCGTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTTGGACCAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGGCC
AATGGCCGAAGAAGTACCCCATGTACAGTGGAGAGAAAGCTACATTCAGGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTTGAAATTCCTCCCATTCGCCGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCATTCTTCAAGCATCCACCAGAGCCTGGCTGA
GGTCTGTGACAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCA
CTTACGGTGTACCCCAACACAGTGCCTTTTCCATGCAGCGCCTGCTGGTCAACCACTAC
ATGAAGAGGAGGCTTTTATCCCGAGGGGGTTCAGTGAATTTGCCTTCCACACCATCCCTGT
GATTGACGGGGCTGGGGGCTGTCTCTCAAAAGGCATGTGCAGAGTGTGTGTCTGGACT
CAGCTGGGAAGGCTGTGGTGTACAGTGTGAAGAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CCGCTGCCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCCCGGCTTAGGCATGACCT
CTGTTTTCTATCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCACTACTAT
GTTTACTATGACACGGACATGACCAGGCGATGGAGCGCTACGTCTCCATGCCCAAGGAAGA
GGCTGCCGAACACATCCCTCTCTCTTCTTCCGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCATTTCCAGGCGCGGTCCACCATGATCATGCTACACCACTGCCCTAGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGAGTGAATGAGACCTTTCAAAAACCTC
CTTTGTGGAAAGCTTATGTCACTGGTCTGAAACTGTTCCCAAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAAGTATCCCACTACCAACCAAGTCTATCTGGCTGCTCCCCAGGTTGCC
TGCTACGGGGCTGACCATGACCTGGGCGCCTGCACCCCTGTGTGATGGCTCCTTGGAGGC
CCAGAGCCCCATCCCCAACCTTATCTGACAGGCCAGGATATCTTCACTGTGGATGGTTCG
GGGCGCTGCAAGGTGCCTGCTGTGTCAGCAGCGCCATCTTGAAGCGGAACTTGTACTCAGAC
CTTAAGAATCTTGATTTAGGATCCGGGCACAGAAGAAAAAGAA**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCAAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCTCTTGACAGTATAAAGCACTTAATTTGGTTCTGATGCCCTGAAGAGAGGCCCTAG
TTTAAATCACAATTCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTTGGATAGCTTGATG
TGTCTATGACGAGCGGGCGCTCTGCATCCCTACCCATGCCTCCTAAGCTCAGTGATCAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTCAGTTC
TGCTCTGAGGCTCTGCTCTCATTATTAGTGTCTACGCTGCACAGTCTACACTGTCAAAG
GAAAAGGGAGCTAATGAGGCTTAACCTAAAACCTGGGCGTGGTTTTGGTTGCCATTCCTATA
GGGTGTGGAGAGCTCTAGATCTCTTTGTGCTGGGTTCACTGGCTCTCAGGGGACAGGAAT
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAAACAGAGGATCCATCAGTTAGTA
GGGTGCATGTGAGTATCATATCCAATTCAATGGAAGTCCCGGCTGTGCTTCTCTTATCA
TCGGGTTGGCAGCTGGTTCTCAATGTGCCAGCAGGGAAGTCACTAGCTGAGCCTCAATCAAGC
CTTATCCACAAATACACAGGAAGGGGTGATGCAAGGAAGGGTACATCAGGAGTCAGGCA
TGCAGTGGTAAAGTGAATACCTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCAGCCAAAGGG
CAGCAGCAGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTACATCAGAAAGAGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCAATTTGCAAGTTAATAGCATGTGTGAGG
TTAGACAGGTGAGTGAATGCAAGCTTGGAAAAATGACTTTTTCAGTTATGTCTTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTGCTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

FIGURE 64

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSESVKRPAPLVTDKARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFQ
EEAIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFH TIPVIQRA
GGAVLT KATVQSVLLDSAGKACGVSVKKGHELVNIYCP IVVS NAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTDMDQAMERYVSM PREAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQ AELKGKRGSDYETFKNSFVEA
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGR LHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

[illegible]

MRVRIGLTLTLLCAVLLSLASASSDEEGSQDESLSKTTTLTSDSESVKDHTTAGRVVAGQIFLD
SEESLESSIQEEDSLKSQEGESVTFEDISFLESPNPENKDYEEPKKVRKPAITAIEGTAHG
EPCHFFFLFLDKYEICTSDGREDGRLCWATTYDYKADKEWGFEDDEEAAKRRQMQEAM
YQTGMKILINGSNKKSKREARYRLQKASMNHTKALERSYALLFGDYLLPQNIQAAREMEFK
LTEEGSPKGTALGFLYASGLGVNSQAKALVYTFGALGGNLIAHMLVLSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCTGGCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

CGCCGCCCGCCCGAGACCGGGCCCGGGGGCGCGGGGGCGCGGATCGCGCGCCCGGGGGCGG
CGGTACCGCGCGGAGCGCAGCGCGCGGGCGCGGGCCGTGACCCCGCGCCCGCGCGGTGACCC
CCATCGCCAGGTTCCGGACAGGCCGACATGACCGCGCGAGCCCTCTGTTGCTGCTCTGTCGCCG
CGCTGCTGCTTGGGGGCTTCCACCGCGCCCGCGCCCGCAGGCGCCCCAAAGATGSGCGAC
AAGTGTGCTTCCACGCGAGGTGGCCGGCTGGGGCGCATGTCGGCGTGCAGTGCCCATGTGGA
GGGGGACCCCGCGCGCTGACCATGTGGACCAAGGATGGCCGCACATCCACAGCGGCTGTGA
CGCGCTTCCGGTGCTGCCCGAGGGGCTGAAGTGTGAACAGATGGAGCGAGAGATGCGCGG
GTGTACGTGTGCAAGGCGCAACCGGTTCCGACCGCTGAGCGTCAACTACACCTCTGCTGT
CTGTCATGACATTAGCCACAGGAGAGAGAGCGTGGGGCCGACAGCTCTCTGGGGGTCAA
AGGACCCCGCCAGCCAGCATGTGGGACGACCGCGCTTCCACACAGCCCTCAAGATGAGGCG
CGGGTGATCGACGCGCCGCTGGGTAGCTTCGTGCGGCTCAAGTCGCTGGCCAGCGGGCAC
TCGGCCCGACATCAGTGGATGAAGGACGACAGCGGCTTGACGCGCCCGAGAGCGCGCTGAG
CCAGGAAGAAAGATGACATCAGCTCAGCTTGAAGAACTCTGCGCGCGGAGGACAGCGCAATAC
ACCTCGCCCGGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTCAAGGTTGGATGTGATCC
GCGGACCGGTTCAAGACCGGTGCTCAGGACGACGACCGCCGTGAACACGACGCGTGACATTG
GAGGCGACCAAGCTCTTCCAGTGCAGGTTGCGACGACGATGAAGCGGGTGAATCAGTGGCG
AAGCGCGTGGAGTAGCGCGCGGAGGCGGCCACAACTCCACATCGATGTTGGGGGCCAGAA
GTTTGTGTTGCTGCCACGGGTGACGTGTGTTGCGGCGCGCCAGCGGCTCTCACTCAATAAGC
TGCTCATCACCGGTGCCCGCAGGACGATGCGGCGCATGTACATTGCTTGGCGCCACCAAC
ATGGGCTACAGTTTCCGACGCGGCTTCTCTCAGCTGCTGCGACAGCCAAAACCGCGAGGCG
ACCTGTGGCGCTCTGCTCTCTCGGCCATAGCTGTGCGCTGGCCCTGGTCATCGGCATCCGAC
CGCGCGCTGTCTTTCACTGCTGGCACCGCTGCTCTGTGGTGGTTGGCAGGCCCAAGAAGCGC
TGACCCCCCGCGCTCGCCCTCCCTTGCCTGGGACGCGCCGCGGGGACGCGCGCGACCG
CAGCGGAGACCAAGGACCTTCTCTGTTGGCGCGCTCAGCGCTGGCCCTGGTGTGGGGCTGT
GTAGGAGAGATGGGTCTCGGACGCGCCCGACACTTACTGGGCGAGGCCAGTGTGCTGGC
CCTAAGTTGTACCCAACTCTACACAGCATCCACACACACACACACACACTCTCACAC
ACACTCACGTGGAAGGCGAAGTGCACACGACATCATCACTCAGTGTAGACGGGACCG
GTCTCAGATGGGACGCGGGGGGCGGGCGGACAGGACGATGGGAGATGAGGACGGAGCT
TCGACAGAAAGGAGGAGGCACATGGCGGAGGAAATGCCAGCACCCAGGACGATCTGTGTG
TGAGGCTAGGCCCTGGACACACACACACACAGACACACTCACTGGATGATGTATGATG
ACAGATGGCGCGACAGTGTCTCTGAAGCGACAGTACGACACGACATGCACAGATATG
CCGCTGGGACACAGATAAAGTGTGCCAAATGCACGACACGACGACAGAGATGCCAGAAAC
TACAAGGACATGCTGCTGAAACACACACGACACACCATGCGCAGATGTGCTGCTGGAC
CACACACACACAGGATATGCTGTCTGGACACACACAGTGCAGATATGGTATCCGGACAG
CACGTGCACAGATATGCTGCTGGACACACACAGATAATGCTGCTGACACACATGCACG
ATATTGCTGGACACACACACACACACGCGTGCAGATATGCTGTCTGGACACGACAC
ACATGTCAGATATGCTGCTGGACACACACTTTCAGACACAGTGCACAGGCGAGATATGCT
GCTTGACACACGAGATATGCTGTCTAGTACACACACACGACGACAGATGCTGTCCGACAC
ACACAGCGATGCACAGATATGCTGTCCGACACACACACGACGACAGATATGCTGTCCGAC
ACACACAGATATGCTGCTCAACACTACACACAGTGCAGATATGCTGCTGGACACACAC
TGTGCACAGATATGCTGCTGACATGCACACAGTGCAGATATGCTGTCCGATACACAG
CAGCACACATGCAGATATGCTGCTGGGACACTTCCGACACACATGCACACACAGGT
GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTCAACTACACACAGTGCAG
TATTGCTGGACACACACATGTGCACAGATATGCTGCTGGACATGCACACACAGTGCAGAT
TGCTGTCCGATACACAGCAGCACATGCAGATATGCTGCTGGGACACACACTTCCGGA
CACACATGCACACACAGTGCAGATATGCTGCTGGACACACGACGACAGTCACTGCTTTTG
GAGGGTGTGCGGTGAAGCTGCACTAGCTGTGCGCTGAGGCTCATAGTTGATGAGGAACTTT
CCCTGTGCTCCAGCTCATCCCCAACTCTGCGCGCTCTGCTCCCGCTCAGTCCCGCCCT
CATCCCGCTCTGTCTCTGCTGCGCTTGGCGGCTATTTTGTCCACTGCTTGGGTGCGCAGG
AGTCCCTCATGCTGTGGGCTGGGTTGGGGCGACAGAGCCCAAGCTGAGAGGCTGGAG
CCCATGGCTAGTGGCTCATCCCCAGTGCATCTCCCCTGACACAGAAAGGGGCTTGTA
TTTATATTTAAGAAATGAAGATATATTTAATATGATGAAGGAAGACTGGGTTCAGGAGC
TGCTGTCTCTCTGGGGCGCGGACCGCGCTGGTCTTTCAGCATCTGTGATGACACACCC
GTCCAGGCGACAGACCCACCCCAACCCCATCTGCTGTGGCGCCGAGATCTGTAAATTTTA
TGTAGAGTTTGAAGTCGAGCCCGGTATATTTAATTTATTTTGTAAACAAAA

FIGURE 70

MTFSPLLLLLLPLLLLGAFPPAAAARGPPKMADKVVPQRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPPREGFWCLNREQ
 RPGQNCNSYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAATYLLTK
 TPKLLTQTDSGDRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQONATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFFVDRLKQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTS EPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRFCVKVRAYRSEFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNYRRTDHEDPR
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPQGSRRASVNPLHEYLVNHLPLAV
 NNDTSEYTMPLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCDFGTS DGSSRIMKSNVGVALT
 FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTCATATTTGGTTTTGGGATCTGCTTTGAGTCCCCTCTTCATTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACCTAGACAAAGATCGCAGATCATAAAG
 AAGCTCTGCTTTAGTTTCCCAAGAGATTACAAAGAAATTTAGAGATGCTATTGTCAAGATCCCTGTCGATTCTATG
 CCGTTTGGGTGGGTGCTCCTCAGGTGATGACGCCCTACCCCTTGGTTTGGGGACATTTGATTGTGTAAAGAT
 CAGATTTACACGGAAGAGGGAAGATTTGGGATTACATGGCTGCCAGCCGGAATCCACGGACATGACAAAAAT
 TCTGAAGGTGAACCTCGATCCTCCGGATATTACCTGTGGAGACCTCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCATTAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGAATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGATATCCCAAGCCTCTCCAGGTTAACT
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCCCTCCAGACC
 AATGATCTCTGGAGAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTTAGAAATCATTTCACAGA
 AGAGTACTCAACAGGGTATACACAATAAGCAAAATATCCACTTTGAATCAAGACAGGTTCCGCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTCAACAGACTGAGGATAAGGCTTTAAAGACAGCCGTTGGGGAATATTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACCGCATCTCAGACATAAAGGTGCGAGGAAGTGCAAGTGTAAATCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCAATGTGAGCACAACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGGCTGCTGTGCCCCGGCCGATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGAGGCTGGC
 AGCTGCGGCTCCGACTGTGGCAGGGCGCGCCCCGCGACGGACCCCGAGCGTCTGCTGCTGCTGACCACTGCT
 GGGAAACCGCCAGCCCCCTGGTGTCTTAGTGTCACTCCAGCCACAACGGACGGGCTGTGCGGTGGGGAAGCA
 GACACAACCCCAACATTTGCTACTAATAGGAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTTAAGTGAATGAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT
 TGACTCCAGAGGAGTTGGCAGCTGTGTATATTATCACTGCAAAATCACATTTGCCAGCTGCAGAGCATATTGTGGA
 TGTGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAACAAATCAACCGACATAAAACATTTGGC
 TACTTACGCTGGTGGCCCTAGTACGACTCCGCCCAGTGTGTGGACCAACCAATAGCATCTTTGCTGTGAG
 GTGCATTTGGGCATAAGGAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTTCTTTGCTGATGTTAGTGTGACCA
 TGTGTAAACGCCCTCTTAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCTTTGTATTCAATGAAGTT
 ATTTTTCTGAACTACTGTAATATGTAGATTTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAAT
 GTATCTAATCGAATCAGCAAGACTGACATTTTATTGTCCTCTTTCGTTCTGTTTTGTTCACTGTGGAGA
 GATTTCTCTGAAGGCAACGACGCTGCTGGCATCAAGAATACGTTACATATAACCAAGTGAATAAGA
 TTCCACCAAGGACATTTCTAATGTTTTCTGTGCTTTAACTCTGGAAGATTTAAAGAAATAAAACTCCTGCA
 TAAACGATTTCAAGAAATTTGTATGCAATTTCTTAAGATGAAGGACAGCCACCAAGCACTTCACTCACT
 TTAAGTATTTCTGTGGAGCTGAGTACATTCAGTTCAGAAATTTAGTTCACGGAAGATGAGTTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTTACAACAGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMAISLYGQLD
TTKKLRDFFVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGCTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACCATGTCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTCGGAGACCCCTGTGGTGGGAATTCACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGAAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACCCGATGCACCTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTCGAGGAGTTTACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAATCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCATGTGAGTGAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCACAAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTCAATGAATCATTATGATTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLIILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS



TGCCTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAGAAAGTGAAGTGGCATT
 TTAACATATGTAAGTTCCTNTCAGATGGAGTGCGAGCTTGGAATAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAATGGGGT

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
CCCGACCTTTAAAGAGTGGGGAGCAAGGGAGGACAGAGCCCTTTAAACAGAGGGGGTGGT
CCTGCCCTTTAAGGGCGGGCGTCCGGACAGCTGTATCTGAGCCCCAGACTGCCCCAGTT
TCTGTGCGAGGCTGCGAGGAAAGGCCCTTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCT
CTTCCCGCTCGTCTCTCCCGGGCCAGGCGACCTCGGCTTCAGTCACTGCTGAGCAGATA
TGGAAGCACTGACTAGCAAGTGTATCTCGTGGCAGAACGCTATTCACGAGAGGATCCG
GAGTGATTATATCAACACTTCTGTGTTGCAACACTGTACATCTCTGCCACATCTTCTCGTA
CCGCTTCAAGAAGCCTGCTGAGTTACCACAGCTGGATGATGAAGATGCCACCTCAACAAGA
TTGGCTCGAGCTGTGACCTTTACCTTGGCAATTGCCCTGGGTGCTGTCTGCTCTCTGCC
TTCTCCATCATCAGCAATGAGTGCTGCTCTCCCTCGCTCCGGAATCTACATCATCAGTGAGCT
CAACGGTCCCTCATCATCAGGCTTGTGAACTTGTTTTCTCTCTCCCAACCTGCTCCCTCA
TCTTCTCATGCCCTTTGCATATTTCTTCTACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTGATGCTCTCTCATCTGCTGGTGCT
AGGATGGTGTGGGTGGCATCAGCACTTGTGGACAAGAACAGGCCAACAGAGATCACTCT
ATGACTTTTGGGAGTACTATCTCCCTACTCTTACTCATGCTATCTCTTCTTGGGTTCTGT
CTGCTCTGGTGTGATCACTGCTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGTCTGT
AGTCAAGCCCGGCTCTGGAAGACTGGAGGACAGGCTGTACTGTCAGCCTTTGAGGAGG
CAGCCGCTGACCCCGAGGATCTGTAATCTACTTCTGCTGGTGCCTTTAGACATGGAGCTG
TTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGCTCTGCTGGAGAAGAGGCCGAAGG
TTCAGCCTGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGGTGCTGACGG
GCCCTGTGTGCTTCACTTGTGGCCATCCATCACTTGGAGCTGTCTCATGATGAGGCTGCCAT
CCCGAGGACTCGAGGGTACTCTTATGGCCAGTCTCTCTTCCAAGCTGGGCTCTTTGG
TGCCGTCACTCAGTTGTACTCATCTTTTACCTAATGGTGCTCTCAGTTGTGGGCTTCTATA
GCTCTCCACTCTTCCCGAGGCTCGGGCCAGATGGCAGCAGACTGCCATGACCGAGATAATT
GGGAATCTGTGCTGTCTCTGTGCTTAAGCTCAGCACTTCTGTCTTCTCTGCAACCTTGG
GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTATA
TTGTGTTCTCTCAACAGCAGCCTTTCAGGCTTACCACACTCTGTCTGTGTGAAGACTTC
ACTGCACTGTGCGGCGAGAGCTGTCCGGGGCTTTGGGCTGGACAGACTGCCGTGCCCGT
CTCCGGTTTCCCCAGGCATCTAGGAAAGACCCAGACCAAG**TGA**CTCCAGCTGGGGTGGGA
AGGAAAAACTGGACACTGCCATCTGCTGCTTAGGCTGGAGGAGGCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGAGCAGGCCATCTGCATCTT
GCATAATCTGAGCCAGAGTTTGGGACAGGACCTCTGCTTTTCCATACTTAACCTGAGCT
CAGCATGGGTGAGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACATCTCA
ATCTGCTCACTGCTTGTCTGGGCCATCCCCATGACCATGTTTACATGATTTAGTGTGCAAT
AGGGTGGGTAGGGCAGGGAAGGACTGGCCAGGAGGCTGGGAGGATAGATGTCTTCC
TTGCTCTTGGCCGACGAGAGCTAAGCACTGTGCTATCTGGAGGGGCTTTGACCACCTG
AAAGACAAGGGGATAGGAGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCCGAGGA
AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVVK
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYIYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPDLMELLHRQVLALQTQRVLLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAVIQVVLI FYLMVSSVVG FY
SSPLFRSLRPRWHD TAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTF TAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTCTCCCGGGCCACAGGGACCTCGGTTCAGTCACTGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTGTGTTTGCACACTGTACATCTCTCGCACATCTTCTGACCCGCTTC
AAGAAGCCTGCTGAGTTTACACACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTGTGTCNTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCTTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAAGTGGACAGTTTGCAAGGACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACCTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCCCCCGGTGT
GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGGAACCATGGCTCCGAGAACCTGAGCACCTTT
GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGTTGCCTCGAAGTGCTCTATAAAGGATATTTAAAGGCCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGAACCTTGATGATCACAAGCCAGGAGAAATTCAGGATCTGGGTG
CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGTTGAAGAA
GGATTAAAGATGGTCATCAGAGCTCCCATTGGAGACATTTTTTACACTTCTTTGGGGATT
TGTTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
AGAAACAAACCTGTGGCAAGGCAGGCTCTGGCAACCGAAGTGCAATTGTGCGCAAGAGAT
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAATGACCCAGGAGGTGGTGTGCGCAGCAAT
GCCCTAATGTCAACTAGTGAATGGAGCACTGAAAGTGAAGATAGAACCTGGGGTG
AGAGACCGCATGGAGTAGCCCCCTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
AGATTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
TGTAACAATGTGACAACTCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACATATCAAGGGCTCTTTGATAA
TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
CAGCTACTGAAACAGGGTCAGTGCAGAAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAAATTTGTCCATTGCAATTCGAAAAGAATGACC
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTAAATGTCTGGTGTGCGCCCTGAGT
TTCAAGAAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAACACAATATAGAGGGTTGGA
GTGTTTAGCAATTCATTCAAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTGTG
TTTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGFGRFQ
MTQEVVCDECPNVKLNEERTLEVEIEPGVRDGMETPFIGEPEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHSRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTA AAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGTCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGACG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTCTGGTGCTGAGGAGCATTGTGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCTGACAGGAGCAGTCTGCAATT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTAGTTTATGCCTCTTTGTCAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTGAGCTTTATTTAGCTACCTAGTGTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAAT
 ACAAGTTGATGATTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCACCCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTAGAAAAGAACATTAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
GGGCTTCTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGT**TAA**CAACA
AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTGTCT
TTTGTAGAGTGCTCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFREFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC
ACCNTGGGCTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAAATTGGTTTAGAAAGAACATTGAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCCTGGATCTTTCTTCCCTCTGGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTTGCCTCAGGGCTAATC
ATCAACACCATTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTCACGGACCCGCGGCCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGTTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTTCCT
GATTCAGTGTGAGGGCACACGGTTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA
TAATGAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCGAGA
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCTCGTGAAGTGGCTGTTTTGGGCCTCGC
TGGTGCTCTACCTTTCTTCCAGTTCCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTTCATGGATGATTGGTGT
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAAATGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTCTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCAAGGGGACAAGTCCCTTTTCATCCTTTGGTGTGAGTTTTCTGT
AACCTTGGTTGCCAGAGATAAAGTGAAGTGCPTTAGGTGAGATGACTAAATATGCCTC
CAAGAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLWPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFATVRSLSRNVS AVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDCSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTTLVN
WLFWASLVLYPPFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGCGGCTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGSTTTCTCTTGGGGAA
 GTAAAAGTGAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTGATCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGACAGGAGCATTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTGAACAACCTGGGTATATAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAAT
 AGTAAAGGATGTAACAGATTAAACGAGAAATGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAATCCAAAAGACCCCTCAGGAGAACATTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCAAATTTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAGTAGCTGTAACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTACGGTCTCCTACA
 TTT**TGA**TCCTTTTAAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTTCAATTTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATTGCTATTAAAAATAAAATGGAAGCAAGAAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLLGVEVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDWRWQFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGAGCAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAAGCCCGCGCGCCACACCCCTCTCGGGTCCCCGCGCGCCTGCCACCCCTTCCCT
 CTTTCCCGCGCTCCCGCTCGCCCGGCAGTCAGCTTGCGGGTTTCGCTGCCCGCGAACCOCGAGGTACCA
 GCCCGCGCTCTGCTTCCCTGGCGCGCGCGCCTCCAGCCCTTCTTCCCTGGCGCGCGCCTGGGCAAC
 GGGGACCGTTGCTGAGCGAGGCGCCAGCTCTACTTTTCGCCCGCGCTCTCTCCGCTGCTCGCCTTCTCCAC
 CAAGTCCAACTCCTTCTCCCTCCAGCTCCACTCGTAGTCCCCGACTCCGCGAGCCCTCGGCGCGCTGCCGTAG
 CGCGCCTTCCCGTCCGAGGTCGCAAGGTGGGACCGCGTCCGCGCGCGCGCAGCCAGGCGACGCTTGCCTGCC
 CGCGCTTCTCTGCACCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AAGTGCAGCGCTTTACGTGTCCAAAGGCTTCAACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCATCATTTGCAAGCTGTCTTTGCTTACGTTTCAAGAAGTTTG
 ATGAATCTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAGAAATGCTAAATGACTCTGGGCTCGCCTCCTGGAGCGGATGTTCGCGCTGTTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCATCGCGGGTCTCGTGACTGTGAAGCCATGTTACAACCTACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCRACCAAGGGGATCTCGATTTTGAATGGAACAAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAAATAGTGTCAAGTGTCTCAGAAGGTTTTCAGGGATGTGGACCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTCCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAAAGCCCAACACAGC
 AGCTGGCAGTAGTTTGGACCGACTGTTTACTGATGTCAAGAGAAACTGAAACAGGCGCAAGAAATTTCTGGCT
 CCGCTTCGAGCAACGTTTGCACAGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGCGAAAGCAGTACCTGTTTCGATGACAGAAATGATTTAGCCAACAGGGCAACACCCAGAGGTCCA
 GGTTCACACAGCAAAACAGACATCATCTCTTCTCAAATCATGGCTCTTCGAGTGTGACCCAGAGATGA
 AGAATGCATCAATGGGAACGACTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAGAAAGAGTGGAAAT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGCTGCGGAGAGTGGCAATGA
 GAAAGCCGACAGTGTGCTGCTGCTGGGCAACAGGCTACCTCTCACTGTCTCTGCTCATCTGTTCTCGG
 TTATGCGAGAGAGTGGAGATTAATCTCTCAAACCTCTGAGAAAGGTGTCATCAAAGTTTAAAGGCACAGTT
 ATCACTTTTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACAAATGTACAGTTTACTATGTGGC
 CACTGTTTAAAGAGTGCTGACTTTGTTTCTCATTGAGTTTGGGAGGAAAGGAGCTGCAATTGACTTGGT
 TCCTGCTCCCCAAACATGTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGATTTGTGA
 TTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTCTGTTTGTGGGTTTTTTTTTCCAACTGTGATCT
 CGCCTTGTGTTTCTTACAAGCAACCCAGGGTCCCTTCTGGCAGCTAACATGACGTAATTTCTGAAATATAATA
 GCTGTACAGAAGCAGGTTTATTATTATCATGTTATCTATTAAAGAAAGGCCAAAGAC

FIGURE 97

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNADAPLHEINGDHLKICPQ
GSTCCSQEMEELKYSLSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSLEFKDLFVELKRYVVGVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYL
AVTGNGLANQGNNEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGGATGAAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTTCTAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGCTCTC
TCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISSLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCTTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTCACTCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 102

GGATGCCAGCGCCTGCAGAGGCTGAGCAGGGA~~AAAA~~AGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTG~~CCATGG~~GACATCCTGGTCCCACCTCTGCAGCTGCTGGTGCTGCTTCTTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGCA~~AAAA~~AGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCA~~ACTTT~~CAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGCTCTGTGCAGAGCCCAAGGAAGTCTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGA~~AAAA~~AGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAAGTTTGCTTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCTGAGGCTACACCCATGCGT
 CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSM DVVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLF FWEHVAE PYGSWAFM
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLP LRG T

FIGURE 104

GTGGGATTTATTTGAGTGAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCCTCATCGCAGG
 CAGATTTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAAGAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGCTTTTGCACCATAACTTCCTCAGCTTGAGCAGTCTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGTCAAACCTGACGGAATGGAACGACAGAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTTACCATCGATCC
 TATGTGGAATGTCGCGCACCTTGGTTCCAGTGCTGGA AACGATATTACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAAACAGAATTTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGAAAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTACGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTTGGTTTTAATTTTGTAACCTGTGGCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDR LGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQG DILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQONITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNHGLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTCTACTTGCCAATTCTGGTTCACGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCAGACAACGGGC
 TGGGC'TCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGT'CGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 GTCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGTTACAGATTCAGGAATGTAG
 GGCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTACGACACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCC
 ATGAAACCTTTAACTTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCGAGCGCAAAGAAG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTTGCCCCTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCA
 GACCCAACAGGCAAATTCACCTAATCCGAGATATACCGAGATCTCAACATATAAGTGAAA
 CAGAATTGAACTGTAAGCAAGCATTCTCAGGAAGTCCGGAAGATAGCATCGCTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAAGATGTGTAGCTAG
 GTAAAGATGACAACTGCCTGTCTGGCAGTCAGCTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT
 GTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAGAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCTATGGGGGAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCTCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGAAGCAAACCTGGAACCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAA

109/330

FIGURE 109

MGA AISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPSPLEPRT



FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTATTTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTGTGATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAA
 TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAGTGGAAATATAAGCCCCCT
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
 TCCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA
 TGACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAAATGCATA
 TACTACAACGTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTTCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCCACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGACAACAAATTAACAATGCAAGGACACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAGA**TACCCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCCATTCTTCCTCAAAA

FIGURE 111

MSGRDTILGLCILALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNPPDPHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

[illegible]

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMO
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSQNRPRADPGIQ
RQDPGAAAFQKPVGADVSLGLVPKEELSTQSLFVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHTNLKTHNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWGGTSTGAAINFALQLFKKSKPNKRKLMLITDGRSYDDVRI PAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

CAGGATGAACCTGGTTGCACTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACCTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTTCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCCTCTCTGAGAATGGCTGAGGAGGGCGCCGAAACTCC
 TCCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACTTACTTTCATGGCGTG
 AACCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGCTGGCGTGGACTCTACTTTGAGTACTTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCCTAGAGTATAACAAAG
 CCATCCGGAACTACACC CGCTTCGATGAGTGGTACTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGGCAGTCTTCCAGTTCCTTGAGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTGGCGCAGAAGCTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGATCCCACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCTGTTCTTCTCTG
 GCGGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATACCCCTCATGGGGAGTGATCCTGGGGGCTGGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGT
 GAAATTTTCAGAAAAACACTGTTAGTTCGGGGCCATTGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTACCCAGAAAACCATGACCAGGCAAGGAGGAAGCTGCCAACAGAAAGGTCCTCA
 CTTCTCAGCTGCCCAGTCAGCCCTCACCTCCAAGTTGGCACTTACTGGGACAGGTTTTCTCT
 AGACTCCTCAT**TA**ACCACCTGGATAATTTTTTATTTTTTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYFSLTLLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQPTGMPYGTVNLLHGVPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMFVFSLEAYWPLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPDTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCCTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGTGCAAAGTCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTAATTTCTGTGCAATACCAAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGTCTACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCAGAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTGTGGCCTACTGGAGGAGGGAGCCTGGTGGCAGGAAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTCTGTCTGGAAATGGCCGGCTGCTCCAGTACTCCTGTTGCCCGGTGG
 TGGTCTCCAGACACCTTGAAAATAACCAATTCACCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAGTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGGCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCAAGCCACACTGAAAATGGGATGTGCATGAACCGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGTGTAAGTACAGAATTCAGCAAATAAAAAGGGCCACCTTGGCCAAAAGCGGTAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSPIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHFPNRRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREPGAEEHV K MVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG
GTTNGCGAACCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCCATGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCAGTGC GGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCGCACCTACAGTGTCTCATTTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCAACTGTGTCAGTGGAGGAGGTGAGCCCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTTCTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAACAAAAATGTGTGGCAA
 TAGAAGTATATCAAGCAATAATCTCCCACCAAGGCTTCTGTAACCTGGGACCAATGATTAC
 CTCATAGGGCTGTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAAGTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTAGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCAGGATATAAATAAAAAATGAAAGTATCCTCCTCAAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKPTWNEFWKYLVPDGVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TCGCGCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGACGGGTGTCGCGTTCCTCAGTTCAGAGAGGTTGGATCG
 CATGTGCTCCACGCCCATCGGAGGCCCTCAGCTACGTTCAAGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTACGTTGACCTTTGCCCAACTCAAGGAGGAGGTGCACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCCTCAAGAAGTGGGCTGCAA
 GGCCCTTGTTTCCCAAGCAATTCAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCAACCCCTGTACCATTCCTGGGTTCCGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCTTGACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGAACCACAGAGAACAGTCCCGTGACATTGCGCACTT
 CCGTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCCAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTCAGGTTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTGCATTCCGGCTGAAGGACGGGGAGGAGACCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCACAAACTACCCCTCACCAATTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTCAAGATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAATAAGAGCTCTCGGATGGGTC
 CGGGAACCTCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCCTGTCTGTCTCTGTGATTGGCATAAAGAGCTTCTGTTTCTTT
 GAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQP GALKSQRLPDLT TVISVDAPLPGTLLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMCMY GATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENS PVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEFPQKTEEAVDQDKWYWTGDVAT
MNEQGFC KIVGRSKDMIIRGENIYPAELEDFHHPKVQEVQVVGVKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGRKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTTCGCGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCCCAC

FIGURE 124

GAGCAGGACGGAGGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCGAACAGATGAAGACAGTGAAGTGCGCCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGTGCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACCTCGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCATGCCAGCGCCAACCACTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGGGCCAGCAGCCCATATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGCTTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCCCACTGACTGGGCTGGCCAGCCCTGTTTTCCAAACATTTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGTTTTGCGGCTTTGGGAAATAAATACCGTTGTATAT
 ATTCTGCCAGGGGTCTTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAFVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

CGGGACTCGGCCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCTCTGACGCTGTCTGGCCCCATGGTCTTGGCCAGTGCAGTGAAG
GAGAAGGAAATGGACCTTTTTCATTATGATTACCAGACCTGAGGATTGGGGACTGGTGTT
CGCTGTGGTCTCTCTCGTGGGATCCTCCTTATCTTAAGTCGACAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCAGGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCCCTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCT
GCCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCTTTGTGGCTACTTGTGTGTGGATGATTTGTGTTTGTAGTGAATGTGGACTGCGTT
CCCAGGCAGGGGCTGAGCCATGTGTTGCTGACCTCCCTCCCCCGTGGCCCTCCATCAC
CTTCTGCTCTAGGAGGCTGCTTGTTCGCCGAGACAGCCCTCCCTGATTTAGGGATGC
TAGGGTAAGAGCACGGGCGAGTGGTCTTCAGTCGCTCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTGTCATCTTCTCATGGACTCCTTCTACTCCTTTAACAAAAACCTTGCTTCCTATCCC
ACCTGATCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTGAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCAGGGGCTTCCAG
AGGAGTCCCCTATCTGCCCGCCCCCTTACAGAGCGCCGGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCTGGGGAATGTGTCCCTGCATATCTTCTAGCAATAACTCCATGGGCTCTGG
GACCTTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCCGTGGTCAG
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGACGCCCTTGGGAACAGTGAGG
GTTGAAGGTCATAACGAGAGTGGGACTCAACCAGATCCCGCCCCCTGTCTGTCCTGTGTG
CCCGCGGAAACCAACCAACCTGCGCTGTGACCATTGCTGTCTGTCTGTCATCGTGATCTAT
CCTCAACAACAACAGAAAAAGGAATAAAATATCCTTTGTTTCT

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVEVQPSGGSLWNLRRLLEPLDANVDA

TOPT-SEDS

FIGURE 128

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCCTGAAGTGGCAGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

129/330

FIGURE 129

MKIPVLPAVVLLSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKADE
FLNWHALFESIKRKL PFLNWDAPKLGKLSATPDAQ

129/330

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTACCCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATC
TTCACATTAATTGTAACGATTAATAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCGTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATAGTACATTGAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVLLTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

131/330
MGVEIAFASVLLTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTGCATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAAACCTTGTGTATGCAGAAATACACCAAAAAC
 CAGGCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAGCAAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCAATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACGAACTA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCAATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCAATAAATCTGTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLFLFLPSAQGRQKESGSKWKVFIDQINRSLENYEPSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

CACCCCTCCATTCTCGCC**ATG**GCCCTGCATGCTCCTGATCCCTGCTGCCCTCGCCTTCTCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGCCACTTCTTGGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGACCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGCACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTTCAGAGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCCCATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCCTCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGCATCCTTCTCGTCTTGACTATGCTGAGTCTATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCCTCTGGCCCTGAAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCAGTGTGTGTGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCTTCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCTCCGGGCCAGCTACAAAGAAACTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTTCTAAATCCTTAACATCCAGGCCCTGGCTGCTTATGCGCAGAGGCCCAATCCATGGACTGAAGGAGATGCCCTTCTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTTCTGAGTTTCAGCCACTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCCCTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCTGAGAAGGAAAGGATGCCCTCTGACCACTCCCCTGCACTGTTACTTGGCTCTGCGCCTCAGGGTCCCCCTTCTGCACCGCTGGCTTCCACTCCAAGAAGGTGAGCAGGGCTGCAAGTTCAACGGTCAATAGCTGTCCCTCCAAGGCCCAAGTTGCTTGCCTACCCTCCCGGCCCTAGTCTGTCACCTCCTTAGGCCCTGCCTCTGGGCTCAGTCCCAACCTTAGTCAAGGGGATTCTCTGCTCTTAAGTCGATGACTTGGGGCTCCCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAAATAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFSTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGCTCTTTTCTGTTTTTCAGAGTAGTTCAACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCTCTGGACTGCTCTCCGAGTAGGATGTCAGTGAATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATT
 CTGGTCATTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC
 ATTCAGGTGGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTATCCTCTAATTGATAATTATTCTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACGTCAGTGGGTGGGTATATATA
 TGTCACAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTGAGTAAACCCATCAAGTTT
 CAAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGAAGTGAACATTATATCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTATGCTAAGGAACACC
 ACATGCCATTATTAAGCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGAAA
 GTGTTAAATAAAGTAGGTACTGTGAAAATTTCATGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTACACTTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAA
 GAAATTAATAGGACCAACAATTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCATTAGGCTGTAAAAACAAAACAAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACGTAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTGTTAAT
 ATTTTACTGTGGTAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAA

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTGGGATTATGGAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACGTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAAT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCTGAAACTAATCGTGTCTAGAAATTGACTTTTGAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCTAGTATTAATTTCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAGGGA
 TTGAATCCGGATGGAAGTCCAGCCCTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCAAAAAGCCCTTACAATGGTGTAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 CCATAAAAGGAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCTCGCTCAGGACATGCGAGGCACAGGCG
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAACTGATTAGGATTGATTTCTTGAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATGTACTTTATTATAGT
 TGTTGATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTAATTTGTTTAAATGATGGTGAAT
 ACTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTACAAGGAAATAAATAACAAT
 CTTGTTTTTTCTAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSHSESPPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSGHGRHR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTGTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCTTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCCTCGTGCCAAAGCTTGGCACGAGGGTGCACCGCTTCTCGCACGCGT**ATGGC**
GGTCCCTCGGAGTACAGCTGGTGGTGACCCGTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCACTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTTTACAGAGGCCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCCTTCTTCTGCTGTGGCCATGTGGTGCAAGTGGTGCG
GGAGGAGACCTCGAGCTGGGCCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGCTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCCTCACCTTCCCAGGCCCTGCGGCTGGC
CCAGACCCACCGGGAGCGCACTGACCATGTGCGAGGACAGACCCATGTGTCAGTTTCTCCTGC
ACACCAGCTTCTGTCTCCCCGTTCATCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
TTCTTGCAACAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGCTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTTGCCAAAGGCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCCCTTCTCCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGTGCTGCCAGCCTTTTCGGCCTTACTTCCACCAGCACTTGGCA
GGCTCC**TAG**CTGCCCTGCAGACCTCCTGGGGCCCTGAGGTCTGTCTTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTCGCGCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGAATCCCC
GGCGTTCCCTTACACACAGTGCCCTGACCCGCGGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCS FARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFS IKMFLT VTRLYFSAEEGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAI R VGLAVVGSVLGAFLTFFPGLR
LAQTHRDALTMSEDRPMLQFLHLSFSLPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FD SGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVS LQYLTPLILT LNCTLLLKT LGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLT PLFLRGV LAYLIWWT AACQLLASLFGLYFHQHLGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

GTTCTTCACATCCTCTCACTCAGAACTCAGACAGCAATATCTTCTTACGGCCCGCGATATTAGCAATGGGCTT
AATCTGAAGGTTTCTCAGTCAAAATCTTTGTGATCTAGTATTGCGGGCATGGCAAGTTTGTCTTAAAGACGTT
TTGGCTGGTTTGGGGCGTTTGACTGCACAGAAGTGGCCAGGAGAATGCGACACACTGCTCGSAGATGAAGG
CGCTTCTTGCTGTGTTCTGGCTTGGCTCAGTCTGCTCACTACATCAATGACAAATGTGGSCACAGTGCATCTCGG
TATTCAAGAATCTTAAAGGTGCTTCCAGTACGCCGTCCAGCAAAAGATGAAGAAGGGCGCTCACAAGATGGCTG
TCAGACAGCGGTGTGGCGAGCTCAGACGACGGCTCCTGCTCCCGAGAGTTTCTCGAGTCCGACCATCTCTTAT
TGACAGACAGCGCTGGCTTAGACAACCTGCTACTGTCTCGGAGAGGACGGGACGACGCAATCAGCCCA
GTGGACTCTGGCCGGAGCAGCAACCAATAGGGCCAGGCCCTTTGAGAGATCCATATTGAAGACAGATCTTTAA
AAAAATAAATCGAGCTTTGAGTTGTTCTTCAAGGACAAAGAGCGGAGTCAGTTGCCAACTGCTCGGACAGCGG
CGAGGAAAAATTTGTAAACACAGCTGCCCTGAAGTTCTTTCAAGTTTTCACCTCATGTTCCAGTGTGTAA
ATTACACAGTCACAGATCAATCGAGTAGATCCAGTGAAGCGCTCTATTAGCTGTGGGGAGTAGCGAAAC
CCCACTGGTCCATATCATATTCAACACCAATATTCTGATGGGTGATGCGCAGAGACGGCCGGCTCATGCGAC
GACACATCATCTAAAGGTCAAACGGGATGGACATCAGCAATCTCCTCAACACTACGCTGTGGCTCTCTCGGG
CAGCCCTCCGAGGTGCTGTGGCTGATGTGATGGTGAACAGAAATCCCGACAGGACAATGAGCAGGCCCT
GGATGCTCAACAGCCCGAGTAGCAGCTTTTATGTGTTTCAACAAGAGTGGCCCGGAGGACAGCTTGGAA
TAAACTGGTGTCGAAGGTTGGATGAGCTGGGTTTTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGA
CATGTTCAGCTTGGAGGAATGACGTGTGTAGCATCAATGAGCATGATCTCGATATGGGACCGCAAGAA
GCGGCTCATCTGATTGAGCCGACGTGAAGACGTGTTCACCTCTGCTGTCCCGCAGTGTGGCAGCGAGGC
TCGACATCTTTGAGGAAGCCGGCTGGAACGCAATGCGACTGTCCCGAGGCGAGGGGAGAGCAACATCT
CCGAGCGCCCTCCATCTCAATAATTCTGTATCAGAGAAGTGGTAAATATCCAAAGAGCCCGTGGTAATCT
CGCGATGACCGCTCGAGGGGGAGCATCAGATAGAATGGGATTTGCCATATGTCATGTCATGTTGAGCGCG
GAGGAGTCATAAGCAGAGATGGAAGAAATAAAACAGTGACATTTTGTGAATGTGGATGGGCTCGAAGTCACA
GAGCTCAGCCCGAAGTGAGGCAATGGCATTTATGAAAGAGAACAATCATCTCGATAGTACTCAAGCTTTGGAAGT
CACAAGATATGAGCCCGAGGAAGTGCAGACGCGCAGCCAGCCGCTGGACTCAACCAACCAATGGCCCCACCA
GTGACTGGTCCCCATCTGGGTCTGTTGGTGGAAATACACCGTGTGTATGATCTGAAAGATATTGTTAT
CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCAATTGAGAGGTTTATGAAGATACAATGAAACAAACCTTT
TTTCAATCAATCCATTGTGGAAGGAACACCGAGATCAATGATGGAAGAATAGATGTGGTGTATGTTCTCTTG
CTGTCAATGGTAGAAGTCATCAGGAATGATACATGCTGCTGCTGCGACAGCTGCTGAAGACGTTTAAAGGA
ATTACTTCAACTATTGTTCTGGCTGGCATCTTTTATAGAACTAGATGGTTCAGAGAAACAGAAAAA
TCAACATAGGCTAAGAGTTGAACACATATATTATTTGCTGCACTTTTATTTTAAAGAAAGAAATACATGT
TAAAGATCGAGAAAGATGATCATCTAATGAAGCGAGTACACCTCAGAAATATGATTCAGAAAAATTA
AAACTCATGTTTTTTTTCAGTGGGAGGATTTCTATTACTCTACAACTATGTTTATTTTCTATTCAT
AAAGCGCTTAAACAAACAATATGATTGTATACCCCACTGAATCAAGCTGATTAATTTAAATTTAAATTT
GGTATATGCTGAAGTGTGCAAGGATCATCAATGCGCAATTTTAAATTTTACAGTCAAAATATTTTAAATGCA
TTGTCGAGAAAGCTGCTCTTTCACTAAACAAGAAATAAATTTTCAAGAGTAAAT

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSP EVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITS IKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLV RKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHD LRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLR RNTAGSLGFCIV
GGYEEYNGNKPF FFIKSIVEGTPAYNDGRI RCGDILLAVNGRSTSGMIHACIARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTT CAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACTCTCAAAGTCAAATTAAATCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFLVVLTFIGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSST
IFDYKHGYIASRVLRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTCTACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACC AACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGGAGCGCAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTIVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCCTTA**ATG**GCGAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTT**CAG**ACTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTGGGGAAGAAA
 CTAAATGTCACAACGGCCTGGAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCAC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTAC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAACAAGATATATCATTTTTCTTCTTCT
 TCTTTTTGTTTGGAAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAATGATATT
 GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTCTTTTAGTAATTTAT
 TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVI PKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSP LGKKLNVT TAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKV VAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSTGTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTTCATTTGAAAAAAAAAAAAAAAAAAAAA

155/330

FIGURE 155

MELIPTITSWRVLLVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

PORT-SE40660

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGCTCA
 CCTCACGGCCCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC
 AGAAGTGGCCCTCCGTTTGGCTCGTGCAGTAACCAAGTTTCAGCAAGGTGGTGTGCACGGCCGG
 GGCCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTG
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTTGGTGGGGCTGGAGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG
 AACTCACAGGTGACGCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATCTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGTGTGGCCGCTGTCTGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGAGCGACCTCGAGACCTCAACATTTCTGAGGGTGGATGGCAGAACCTTAAGTGT
 CGGACTCCCCCTATGTCTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC
 TTTTCAGACACTGGGGTGTACATGCATGGTGACCAATGTTGCGAGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACACGCGAAAGTACAAGCCTGTCTCTA
 CCACGTCCACTGGTTACACGGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGGACACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCGGTGATCAGGTGAGGGGCGAGTGTGCTGCCACAATT
 ATGACCATATTAACATAACACCTACAAACAGCACATGGGGGCCACTGGACAGAAAAACAGC
 CTGGGGAACCTCTGCAACCCACAGTCACCACTATCTCTGAACCTTATATAATTTCAGACCCA
 TACCAAGGACAAGGTACAGGAACTCAATA**TGACT**CCCCCTCCCCAAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
 RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAENGLAS
 LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
 ISEGAFEGLFNLYNLGMCNIKDMPNLTPLVGLEELEMNGHNFPEIRPGSFHGLSSLKKLW
 VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHNPWNCDLW
 LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
 KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTlnfshvllSDTGVYTCMVTNVAGNSN
 ASAYLNVSTAEINTSNYSFFTtvtvETEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
 TTRVPKQVAVPATDTDKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLRKRHQORS
 TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPtIHDHINYNTYKPAHGAHWTE
 NSLGNLHPTVTTISEPYIIQHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKACLAGYTQRCENLLEERNCSDPGGFVNQYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSFQESHITVAGWNVLADVRSFGFNKNDTLRSG
VVSVDLSLLCEEQHEDHGI PVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLGLVSWSYDKTCSHRLSTAFTKVLPPFKDWIERNMK

ACACGAGCATTTGGTATCTTCAGTTGTGCATCAAGTCGCAATCAGATTGGAAAAAGCTCAACTTGA
AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGC
TTCAACCTGACTTTCACCTTTCTTACA AATTCGATTACTGTTGCTGTTGACTTTGTGCCT
GACAGTGGTTGGTGGGCCACCAGTA AACTACTTCTGGGTGCCATTCAAGAGATTCTTAAAG
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
AATGAAGCATCCACGAAGAAGGTAGAACTTGACA AACTGTCCTTCTGTGCTTCCTTACCTCA
AGGCCAGAGCAAGCTCATTTTCAAACAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
CCAAAGTGTCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTTACAGAGGGTCGCCATC
CTCGTTCCCACCGGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTA AAAAGT
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCAGCTGGGTACAGGTTACGTTACAGTG
GATATTTTGGGGGTTGTTACTGCCCTAAGCAGAGAGCAGTTTTC AAGGTGAATGGATTCTCT
ACAACACTACTGGGATGGGGAGGCGCAAGCATGACCTCAGACTCAGGGTTGAGCTCCAAAG
AATGAAAAATTTCCGGGCCCTGCCTGAAGTGGGTAAATATACAATGCTTCCACACTAGAG
ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
AGAACAGATGGTTGAGTAGTTGTTCTTATAAATAGTATCTGTGGAACACAATCCTTTATA
TATCAACATCACAGTGGATTCTGGTTTGGTGCATGA CCCTGGATCTTTTGGTGATGTTTG
AAGA AACTGATTCTTTGTTTGCATAAATTTTGGCCTAGAGACTTCAATAGTAGCACACATTA
AGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTTCTCTTTTGATTTTCTTAGCAGAGCT
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
AGGGTTAAATATTGTAATATGGATACCTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCA TTTATCCTGTACAATCATCT
GTGAAGTGGTGGTGT CAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCCGCTGCAAGGAC
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCTCTTACAGGAGGAGGACTGCCAGATGATGCC
TCCAGTGATGCCACAGAGAAATACATTCTCTATTAGTTTTTAAAGAGTTTGTGTAATGTA
TTTTGTACAAGTAGGATGATAAGATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
TGTCTATCAATACTCTGTAGTAAAATGTGAAAAGGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWGWGGEDDDLRRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCA**AATG**
 GCCAGGCGAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCCTGCCTCTGCCCTGGGC
 CCGGGCAGGGGTGGCCGCGAGGCTGTATGAACCTCAATCTCACACCGGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGTGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTTGGCA
 GATGGAGAAGGGTCTAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTTCCGG
 TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCTCCCCATCAGAGTTCTCGTGGGGGACCTTGTGTACCCAGAACACTTCCCTACC
 CTGGCCCCAGCTCCTATCTCACTAAGACCGCTCCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTCGGGGAGCGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCAACCCTGAAGCT
 CAAAGTGGTGGCGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCCCTCGCTGAAGCTCGAGGAAACCCCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
 TGCTTCAGCATCCGGGCCGAGAATAATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGTACACTTATCACTGTGA
 GTTTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTGTGT
 GGAGACTCCATCTGAGTACCTGGAAATTTGCTGTGAGAACCCGGCTGCTCCCGCCCTCT
 ATAAGTCTGTCAAAACTTACACCGT**GTGA**GCATCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCATT
 TGGGTGGGGCTGTGGCCTGGATCATCCATCCATCTGTACAGTTACGCCACTGCCACAAGCC
 CCTCCCTCTGTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGTCAGGACT
 TGTATGCTTGGGGTGTTCGCTGTGACTCCTAGGTGGGCTGGCTGCCACTGCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGGTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCTATAAGGGTTAAAAATCCATAACTAAGGTTGTAC
 ACATAGTGGGCACATCTACAGAGAGAAGTGTGCATGTACACACACACACACACACACA
 CACACACACAGAAATAAACAACATCGCTACATGGGCATTTAGATGATCAGCTGCTGTA
 TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACTAGAGCTGAAAGGAAATTTGACCTTCA
 AGCAGCCCTGACAGGTTCTGGGGCCGGGCCCTCCCTTTGTGCTTTGTCTGTGAGTTCTTGC
 GCCTTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACGTAGTATTGACAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG
 AAACCTTTCAGTGAGGAAAAGGCCCTTGACGCGGTAGAAGAGGTTGATCAAGGCCGGGCGGG
 TGGCTCAGCCCTGTAAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCAGAGATCAGGA
 GATCGAGACCACCTGGCTAACACGGTGAACCCGCTCTACTAAAAAATAACAAAAGTT
 AGCCGGGCGTGGTGGTGGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCAACCCGGGAGCGGAGCTTGACGTGAGCCAGATGGCGCCACTGCACTCCAGCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHPGEFPVSVVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFDGTQ
MVTEDSVVYYNYSIIGTFTVKLVVAEWEVEPEPATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTFRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCMCCGPFLETPSEYLEIVRENNHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
 GGGCCGCTTGGCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
 CAACAGACGGGACAACTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
 GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT
 GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG
 CCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
 TGGCTGGTTCTTTGTTTCCAAA
 AA

165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCCHRSKCGMCCCT

165/330
MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCCHRSKCGMCCCT

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGCCTCTTACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACAGCTTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACCTGCTGAGCAGAACCAATTATACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACAGGGGGACTCATGGGTGTGATTAGAGAGCCATGGTGAAAGCCGTG
 CCCACACGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAAATTTGGAGCCACAGTTTACCC
 TGTGTGATCAAGATGACCCCTCAATTTGGCGATGCCCTTCTGGAACAGCAGCAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGC
 CATTTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGGTTTCGCCGAGCCGCGACGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTGTGTCTAGAGAT
 GCGGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCTATCTGCAGGGGCTTTACGAAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGGCGCAGGTG
 GCGCGTGACTGGGCCATGGGGAGAAGCTGTGTTTCGTACTCCAGGCTAACCCCTGAACCTCCC
 ATGTGATGGCGGCTTTGTTGAATGTGTGCTCGGTTTCCCATCTGTAATATAGTCGGGGG
 GAATGGTGGTGATTCTTACTCACAGGCGTGTGTGGGGATTAAAGTGCCTGCTGGGGTGAGTGA
 AGGACACATCACGTTTCAGTGTTTCAAGTACAGGCCCAAAAACGGGGCAGGGCAGGCCTGAG
 CTCAGAGCTGCTGCCTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
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FIGURE 167

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
 RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
 TIMDDEVTKRFSAEELSWNLLSRTNYNFYISLRLTVLWGLGVLI RYCFLLPLRIALAF TG
 ISLLVVGTTVVGYPNGRKFKEFMSKHVHLMCYRICVRALTAIITYHDRENRP RNGGICVANH
 TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
 DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
 LRMMTSWAIVCSVWYLP PMTREADEAVQFANRVKSAIARQGGLVDLLWDGGLKREKV KDTF
 KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCTGGGCTGGCTCCAGACACCTTTGA
CGATACTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTAAGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCCTCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGAGAAGAGCGGGGCTGT
GTGCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTGAAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAATCGGTTCGGACCCAGCCCTAGCAGCCTTCTCCCCAACAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTATTAATGGTATTGCAGTGTGA

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVYGCAEEMEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGKAQNGIAIMVYTNSSNTLYWELNQAVRTGGSGREL
YMRHFFPKALHFYLIRALQLLRSGGCSRGPGEVFRGVSLRFEPKRLGDSVRLQGFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLTLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCTCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCTCTGTGTCTCTGTTGGTGCCCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFFDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPKVTMGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
 TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
 CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAC
 AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
 GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGATGACTCAGGGATCTACTATGT
 GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
 AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
 ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
 GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCTCCCATCTCCTGGAGATGGGGAG
 AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCC
 ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCT
 GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGACTGGGGCTATTTCTTTGGTTTC
 TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA
 ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
 TAGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
 AGATGGAATAATCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
 AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT
TTTTCATGAAATTATTCTCTCTCCTGTTCAATAAATGATTACCCTTGCACTTAA

174/330

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

174/330

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTtaggtctattgct
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

MTTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWFFPGIIGAGLMA
IPATMTSLTARKACNNRTGMFLSSFFSVITVIGALYCMLSIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGRASSFHFDSEENKHL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

GTTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCAGATCAGATATCTTTTAAAGAAACGACTCTCATTGAAAAAGTCTTGGTGGAAA**TAG**TGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGTTTCAACAGTTGCTTTAATAAATCACTTGCCCTGC

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

178/330

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

180/330-180/330

GGAGAAGAGGTTGTGTGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
TGGCTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGCTCC
AGTGTTCCTCCACAGCCCCAAACGGAACGTGGTTTTGGGGTACCTGGGCTGATCACTCCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
CCAATGCCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTTGAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
GCCCCGCTTCCATTTCAACATCCTGAAGTCTTATATAACGATCTTCAACAAGAGTGCAAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCTGCTGGACATGCTTTGAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCAATTG
TCAGGAGAGGCCAGTGAATATATTGCCACCATTCTGGAGCTCAGTGCCTTGTAGAGAAAA
GAAGGCAGACATCTCTCCAGCAGCATGGACCTTTCTGTATTACCTCTCCCATGACGGCGCGCG
TTCCACAGGGCTTGC CGCTTGGTGCATGACTTCACAGACGCTGTCATCCGGAGCGCGCTCG
CACCTCTCCCACTCAGGTTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
ATTTTCATTGATGTCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
CTGGTCTGTACAACCTTGCAGAGGCCACCCAGAATACCAGGAGCGTGCCGACAGAGAGTGTC
AAGAGCTTCTGAAGGACCGCGATCTTAAAGAGATTGAATGGGACGACCTGGCCCAAGCTGCC
TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGATCCTGAGGTCTACGAC
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACTCTGGAGCTTTTATTCCTTTCTC
CGCAGGGCCCAGGAATGCATCGGGCGAGCGTTGCCATGTCGGGATGAAAGTGGTCTCGG
CGTTGATGCTGCTGCACATCTCCGGTCTCTGCGACACCACTGAGCCCCGAGGAAAGCTGGAA
TTGATCATGTCGCGCCAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTCTGCAAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPCKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMEFHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDFFKDKAKSKTLD FIDVLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATGT**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC
AGTGTGGAGAAAACTAGGCAAACCTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTCACAAAAAAAAAAAAAAAA

184/330

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTT CAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTTGCTCCGCACGGACCCAGATGTCAAGAAT**ATG**AACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTAGTGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAAGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTTAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCACTAACCA
 AACAACCTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGCCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCCACCAAGA
 GCCTCCTTGTTTCATAACCACAGGTTACCTTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTATCAGCTTCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTGTCTG
 CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTCACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACTGCTGCATGGCGTGGCTGTCAACCACCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAGAAGCAGTTAGGTCTCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNSTQEVVQYNWETGDDRF'SFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGpchptLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPClWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTCLE
LWLGLLHGLALLHLLHGvGCHHLQHvHQDGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCAGATGTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTATTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCCTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCTGCCCCGCCGTAGATTGAG
GACATTCGCCCTGTGTGCCACCAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAATTTCTCTAACACTGAAA

FIGURE 192

MWLPGLLSLCLSPILSSPSLKSQACQQLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCGGCTGCCGCTGCTGCCGCCGCCCTCGGGTCGTGGAGCCAGGAGCGACGTCA
 CCGCCATGGCAGGCATCAAGCTTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGATGTGCCCTTCCAAATATACAACAATACTGGCCCTCTTTGTCTATTTTTTACATCCTTTCACTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAAGAACTTGGCATCTTTTC
 TTACAAOCCGCAATTCGTGTGCTGACGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGA
 GCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTTGCACATATACTAGGCTTTTTCTTGGTCTTTGGAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAGAAATTAAGCTGCTGAATGGTATAGCAAGCTCTTGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACATTTTTACAGAGACTTGTCTGAAGATTAAAGGATTTTTCT
 CTTTTGGAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTTGGTGTCTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTAGGTTGATTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTTAAATTAAT
 TAGCCTCCATTATTACAAAAAATTATAAAAAAAGTTTTTCACTGAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACCTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAAGTGTAATGCCCATGCCCTCCGTTAAGGGTGTGGTTTTACTGGTAGACAGATGTTTTTGGGATG
 AAAATTATTTTTATGGAATTGCTACAGAGGAGTGCTTTCTCTCAATTTGTAGAAGAATTTATGTTAAACTTTA
 AGGTAAGGGTGTAAAAACATTTTGAGATAAGGTTTTTATTTATGTTTATTATTTGTTAGAGTGAGTGCAATGT
 GGGAAAGAAATGACATTTGAAATTCAGTTTTTGAATCCTGTTCTATTATAAGTGAATTTTGTGATCTCCTATC
 AACCTTTCATGTTTTACCTGTAAAAATGGACATACATGGAACCACTACTGATGAGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAACCTTCTCTGCTTCCCTTTTGAATTTATTTGGTATGTTATATATACATAAAAA
 TAACTTTTCAAATATAGTTTAAACACTTGAAGTGTCTTACTTACCTGGAAAAATTTGCTATGCCGTACATT
 CAGAGTGCCCTTCCCTGCAAGGCTTGGCATGATTAAACAGTAACTTGTAGCTTACAGATAATTCATGCA
 TTAACAGTTTTAAGATTTAGACCATGGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTAAAGCAAGTTTCTGTATACCTCTGAAGCTGTTTGAATTTTGAAGTATCATCATGATAGATCTGCTGTTT
 CCTTATAAAAGGCAATTTGTTGTGAGTTTATGCAAGTAGCCAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCAGTAACAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAAATATCAGGA
 CTTTTTTCAGAGTGGGTTATAAAACATTTCAAGTTGGTCTGACAGTATTTTGTAAAGATATTTGTTGTATG
 TTTATTCAGTATACTTACATAAAAAATTTTCGCCATCAGCCAAACCTCAGTAATCATGACAGCTGTCTGTGT
 TTTATGAAGTTTATTTCTCAAGAAATGGGAATAAATTTGGGATTTGTTGAGCTTTTTTACTAAAGATGCCATA
 AGCCACAGGTTTTATTGCTCAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAATAATCG
 CGCTGTGGCTGGAGCTTCCCACTGGAGGCTGAAAGTGGCTTGGGTAATTATAAGTTTCAGATTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGCTGAGACAGTTGGGAACCTTTGTGCTGTGATCTACTGGACTTT
 TTTTTTCAGGAAGTGACTTCTGTTCCCTTCCCTATTTCTGTTCTGGATGCTGAGTCAGTGACCTGCACTT
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCTGCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 GTGCTTTGACCTTGTATACAGCTTGACATAGTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATGCTAGTATACCAATACCTATTCTCTATGGAAGAAAACTTTTGTATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAAATAA

FIGURE 194

MAGIKALISLSFGGAIGMLFMLGICALPIYKNYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVSAFGLPIVFARAHLEIWGCALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPFNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLELHLEHNDLVKNFAHFPRLLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEP TSG
HLLSAVTNRSDLGPPASSATT LADGGEGQHDGT FE PATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQC FVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
LEGALVIINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCAGCCAA
CTGGAGCCAGAACC GGACCCCGTGCGCCGGCGCGCCGTTGAGTTCCCGCGGACAAGATGG
TGTCACTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGACGGTG
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLPGASPVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

[illegible]

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGTTCTCCAGTACCCCTCCCGCGTTACCCGCGGGCGG
 CCGAGGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCCAGGGT
 GGGAGAGAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAATAGACTTCGAATTTATCTTGGTGCTCTCATACTTGCCTGCATCGTCTTTC
 AACCCCTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTGATGGATTCCGTTGGGATTACT
 TATATAAAGTTCACACGCCCCATTTCATTATATATGAAATTTGGTGTTCAGCTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCCTAACCATTTATCTTTGGTAACTGGCCCTCTTTCAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCCGAAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTTT
 GGGAAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTGAAGATAG
 AGTTGCCAAAATTTGTAATGGTTTACGTCAAAAAGAGCCATAAATCTTGGTCTTCTATTTGGGAAGACCCGTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTCAGATATTGACAAGAAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG
 AATGACGCGAGTGCTCTGAGGAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCACTATACCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCACATTTTACAGAATAAGTCAGATGACTTCTGTTAGGCAAC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTTCAGAAAGAATTTT
 TCAAAAGAAAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGCTCCTTATACACAGATA
 CTATACTCCTCCTGGTAGTGTAAACCAGCAGAAATAGACCAAGAGGGGTATACCCCTATTTCATAGGGGTG
 TCTCTTGGGCGCATTTATAGTGATTGTATTTTTGTAAATTTTCATTAAAGCATTTAATTCAGATCAAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTTATACAGCCCTAAAGTTACTTTGAAGTGGATTGTCATA
 TTGAAGTGGAGATTCCATAAATATGTGAGTGTTTAAAGGTTTCAAAATCTGGGAAACCAAGTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACAGGACCAAA
 ATACTTACACCTGCAAGGAATTAAGATGTGAGATATGTCCATTTGTTCACTGTACATAGGATAGATAAG
 ATCCCTGCTTTAATTTGGAGTTGGGCGAGATAATGTATATATTTAGCAACTTTGCACATATGTAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCCTCTGATGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGCTTATAAC
 TTGATTGAAATGACAACTTTTGCACCCATCTCACAGATACTTGTACCGCATTTCTCAACTGAAGGAATTT
 TCTAATAATCCGGAATAATGAACATAGAAATCTATCTCATAAATTTAGAGAGAAGAAGCTGATAAGTGTGA
 AAATTAATATGTATAACCTTTGAACCTTGAATTTTGAGATGTATTCCCAACAGCAGAAATCCAATGTGGCAT
 TTCTTGTCTAATTTCTTCCACAGAACGTGGTTTTCAATTTTTCCTTCAAAAGAGAGTCAAACTACTGACAG
 ATTCTGTCTAATATATGTTTCTGTCAATAAATATTGGAATTTCTGTATGAGTCAATATTACTGTGATTTTCA
 TAATATGAGAGACCATGATATACTTTTCTTATATAGTTTCAAGCAATGGCCTGAATAGAAGCAACAGGCA
 CATCTCAGCAATGTTTTCTCTGTTTGTAAATTTTGTCTCTTTGAAATTAATCACTATTAAATACATTAA
 AAATCAATTTGGATAAAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGCGGGAGGCCAG
 GACAGGCCCCACCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCTTGCCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAAGTACAA
 CCAGATCCAGAGGCAACAGGGACAATGGCCACCTGGGACGAAAAGGCAGTACCCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGCTGTGGCGGGTGGCCCCGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAAGACGGCAACTCTTAAGGTTAAAAAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTGAGTCTGCTCTGAGAAGCCCCCTGGACTTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAACCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAAGCTGACAGTCACTGGCCAGTTA
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAAATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGLRKLFSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSFTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCAGCAGGCCGCCAACAT
GCTCTGTCTGTGCCTGTACGTGCCGCTCATCGGGGAAGCCAGACCGAGTTCACGATCTTTG
 AGTCCAGAGGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCCCACTACCGGCAGTGAAGCAGAAAAATTTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCGAGCTAGACTTTGAAGAAATTTGTCCATTATCTCCAAGATCATGAGAGAAGCTGA
 GGCITGTTGTTAAGATTTTGGACAAAAAGATATGATGGACGCTATGACGCGCAGGAGATCATG
 CAGTCCCTGCGGGAGTTGGGAGTCAAGATCTGACTGGAACGAGTGGAGAGACTACCACTCCTCC
 CATGGATAAAACGGCAGCATGACCTGCTACTGGAAGCATTTCCAGTATCTTTGATGTG
 ACCCCGTGGAAAAATCCCCAGATCATCTCTACTGGAAGCATTTCCAGTATCTTTGATGTG
 GGTGAGAATCTAACGGTCCGGATGAGTTACAGTGGAGGAGAGGCGAGCGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGCGAGGGGCCGTATCCAGAACCTGCACGGGCCCTGG
 ACAGGCTCAAGGTGCTCATGCAAGTCCATGCCTCCGCGAGCAACAACATGGGCTCGTTGGT
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGGCCAGGTCATCTGGCGGGGCAATGGCATCAA
 CGTCTCAAAATTTGCCCCGAATCAGCCATCAAATTCATGGCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACCGAGAGACTCTGAGGATTCACGAGAGGCTTGTTGGCAGGGTCTTTGGCA
 GGGGCCATCGCCAGAGCAGCATCTACCCAAATGGAGTCTCTGAAGACCCGGATGGCGCTGGG
 GAAGACAGGGCCAGTATCAGGAATGCTGGACTGGCGCAGGAGGCTTGTTGGCAGAGAGGGGG
 TGGCGCGCTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCCATGCCGCATC
 GACCTTGCAGTCTACGAGAGCGCTCAAGAATCTGCTGGCTGGCCATGTCAGTGAAGCAGCG
 GAGCCCGCGGTGTTTGTGCTGCTGGCTGGCCATGTCAGGACCATGTCAGTACCTTGTGGCCAGCTGG
 CCAGCTACCCCTGGCCCTAGTTCAGGACCCGGATGCGGCGCAAGCTCTATTGAGGCGCTG
 CCGGAGGTGACCATGAGCAGCTCTTCAAACATATCTGCGGACCGAGGGGGCTCTGGGCT
 GTACAGGGGGCTGGCCCCAAGCTTCTGAAGGTCTACCCAGCTGTGAGCATGACGTACGTGGT
 TCTACGAGAAGCTGAAGATCACCTGGCGCTGCAGTCCGCGT**T**GAAGGGGGGAGGGGCCCCCG
 GCAGTGGACTCGCTGATCTGGGCCGCAGCTCGGGGTGTGACGCCATCTCATTCTGTGAATG
 TGGCAACACTAAGCTGTCTCGAGCCAGGCTGTGAAGCCCTAGACGCACCCCGCAGGGAGGGT
 GGGGAGAGCTGGCAGGGCCAGGGGCTTGTCTGCTCAGGCTCAGCAGGCTCCGGGCTCAGTGTGTAA
 AGGGAAGACCAAGCAGCATTCCTTAGGCTCAGGCTTGAAGCTGGAGGCTGGAGGCGGCTTAGT
 TCTTCCATTTACCTTGCAGCCAGCTGTTGGCCACGGCCCCCTGCGCTCTGGTCTGCGGTAGC
 ATCTCCCTGGCCCTCTGCTGCTGCTGCTGCTGAGGTAAAGTGGGAGGAGGGCTACAG
 CCCACATCCCACTCTGCTCAATCCATAATCCATGATGAAGGTGAGGTACGCTGGCCT
 CCCAGGCTGACTTCCAACTACAGCATTGAGGCCAAGCTTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCTTTGGTCACTGGCATGAGCCCTGCTGATGGCTGGGGCTCTGGGCACTGT
 TGGAGTGCAGGGGCTGGGCTGGCTGGCTGCACAGAAGCGAAGTGTGGGGCTCA
 TGCTGCTTGGCTGGCTGGCCCTGGACCTCTCAGGATGGGCCCCACTCAGAACCAACTCACTG
 TCCCACTGTGCACTGAGGCGAGTGGAGCACCATGTTGAGGGCGAAGGGCAGGCGTTTGT
 GTGTTCTGGGAGGGAAGGAAGAGGTGTGGAGGCTTAATTTATGACTTTGGGAAAAGGG
 TTTTGTCCAGAGGACAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGCAGGAG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGAGCGCTGGGGGTTCTGTGCCAAC
 CCAGCAGGGCGCAGCGGACAGCCCACTTCCACTTGTGCTACTGTTGGAACTTATT
 ATTTTGTATTTTATTTGAACAGAGTTATGTCTTAATAATTTTATAGATTTGTTTAAATTAATA
 CTTGTGATTTTCAAGTTCATTTTATTTATTTATTTATGTTGATGTTGATGACCTTCC
 AAGCCCGCCAGCTGGGATGGGAGGAGGAGAGAAGGGGGGCTTGGGCGCTGCAGTCACT
 CTGTCCAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGGACCTG
 GCTCCTTTCTCTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCTTAGGATTTACGGGTTTGA
 CTGGGGCGTGAGAGAGAGGAGGAACCTCAATAACCTTGAAGGTGAATCCAGTTATTTCT
 CTGCGCTCGAGGGGTTTCTTTATTTCACTCTTTCTGAATGTCAAGGCAGTGGAGTGCCCTC
 CACTGTGAATTTGTGTGGCGGGGGCTGGAGGAGAGGTTGGGGGCTGGCTCGCTCCCTCC
 CAGCTTCTGCTGCCCTGCTTAACAATGCCGGCCAACTGGCGCACTCAGGTTGCACTTCC
 ATTCACCAAGATACCTGATGAGGAATCTTCAATAGGATCAAGATCAATGCAAAAAAT
 GTTATATATGAACATATACTGAGTCTGCAAAAGCAAAATTAAGAAGAAATGGACGTGAG
 AAGTTGCTATTTAAGCAGCTTCAATAAAGTTGTTTCAAAGCTGAAAAAATAAAAAA
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FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIQSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPVDEFTVEERQTGMW
 WRHLVAGGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI
 NVLKIAPESAIAKFMAIEQIKRLVGSQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG
 CAATTGCACTCATCTTGGCTTTGGTATTTACAGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAAGATGAGCTGTGCGAGCAGGATGAAATGTTAGAGGCCGGACAGCAGTGTTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTCGGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGCGGGAG
 TCACCTACAGCTGTAAACTCAAAGGCTTCTCTGTGTGTCTTCTTTCTTGGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAACAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCTGGAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACCCGATTTTATAAATAAAGTGAACACCTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGATAIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIIITSKGKGANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVNTSFELENSENVMTKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK



FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFL
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 211

CTTCGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACATGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAAGTGAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACTTTTCAATTTTGAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCCTCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTGCTGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTGAGTAACGCCACCTGTGAGTTCCTGTCTGGTGAAAACAAGACTCTTGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTCG
 GGGACTGCTGCCCTGAGGTCCCTGGGGCTGCACCTTGGCCAGCACCCTTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCCTCTTCCCTGCTCTGCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGTGCCTTGTCTTCTTATTATTA
 AAGCACTGGTTCAATTCATTCGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTCACTGGCCACCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG
GCGGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGC GGGGGCCCCAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
CTACCGGAGCACCGCCCGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCACCGCTGGTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCACCCACAG
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCACTGT
GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCCCTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTTGGAACGGGTCA
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTAGTACAGAAAAACAAACTGGAAAA
CACAA

FIGURE 214

MVPAAGALLWVLLLNLGPRAGAQGLTQTPTTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGFAAAELLAATVSTGFSRSSAINEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCCPALA
FWKRVRIGLEDIWNLSVFTTEMQPIDRNQR

FIGURE 215

CCGGGTCGACCCACGCGTCCGGGGAGAAAGGA**ATG**GCCGGCCTGGCGGCGGGTTGGTCTGTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGGTCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGGCAAGAGCA
 GAACCTGCTTGGGGGCGCTCTGAATCACTTCCGCTCCCGCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCCGGAGCACTGTAAAGTATGAGTGATGTGGGTCAACGTTGGGCTCTACCTCCAGGAGGTCACAAAGTGCCT
 CAGTTCATGGCAAGTGGGCCTTCTCCCGGTTCTCTGTTCTTCAAGAGCCGGCATCGCCCTGGCCCTCGTTCT
 CAATGGCCTGGCCAGCTTGGTATGCTCTGCCGCTACCGCACCTTGTGCCAGCTCTCTCCCCATGTACACACA
 CCTGTGGGCTTCCGCTGGGTGTCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGACACTGCAC
 CTCACAGAGAAAATGGACTACTTCTGTGCTCCACTGTATCCTACACTCAATCTACCTGTGCTGGTCAAGGAC
 CGTGGGGCTGCAGCACCAGCTGTGGTCAGTGCCTTCCGGGCTCTCTGCTGCTCATGCTGACCGTGCACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGAACACAGCGGCGGCTGCCTCAGCTGCAGCAAGTGGTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGCTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGTCCTCTTTTTAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTgaAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC
 GCCCTGCTGGCTCCCTTCTCCCTCAACCCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTTGGACATGA
 AGGATGTGGGCCAGAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCACGATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCTGGAGCTGAACCTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCTGTTTCTCCACACAGCCTCTCCCCACATCCCCAGCTG
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACACGGGACACAGGCTTAGGGATACAGGGGGTCCC
 CTTCTGTATACACCCCCACCTCTCCAGGACACCACTAGGTGGTGTGGATGCTTGTCTTTGGCCAGGCCAA
 GGTTCAGGGCGATTCTCCCATGGGATCTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCTGTGCTGCTGCTGGTTGAGAGCCTGCCACCGTGTGTGGGAGTGTGGCCAGGCTGAGTGCATAGG
 TGACAGGGCGCTGAGCATGGCCTGGGTGTGTGAGCTCAGGCCAGTGTGCGAGTGTGGAGACGGTGTGTG
 CGGGGAAGAGGTGTGGCTCAAAGTGTGTGTGTCAGGGGGTGGGTGTGTAGCCTGGGTAGGGGAACGTGTG
 TCGCCTCTGCTGGCCATGTGAGATGAGTGACTGCCGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCTGTCAACATCAATAATCACTTGTGGAGCGCAGCTCTGCCAAGAGCGCACCTGGGGGAGAGC
 CAGGAGCTCTCCATGGCCAGCTGCTGTGTGATGTCTCCGTGCTGCTGCCCTTGGCCGCTCCTGCAAC
 CTCACAGGCTCCCCACACAACAGTGCCTTCCAGAGCAGCCCTCGGAGGCAGAGGAGGAAAATGGGATGGC
 TGGGGCTCTCTCATCTCTTTTCTCCTTGCCTTCGCATGGCTGGCCTTCCCCCCTCAAAACCTCCATTACCT
 GCTGCCAGCCCCCTTGGCATAGCTGATTTTGGGGAGGAGGAAGGGCGATTGAGGGAGAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTCTTCCCTTCCAGAGGGTCTTACTGTTCCAGGGTGGCCAGGACAGCAGGGGCC
 ACACATATGCTGTGCTCGGTAAAGGTGACCCCTGCCATTTACAGCAGCCCTGGCATTTCTGCCCCACAGG
 AATAGATGGAGGAGCTCCAGAACTTCCATCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGT
 CTCTGCCCTGAGCCCTTGTCCCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGTG
 GCTCGCTAGCTTCTTTGATACTGAAAGCTTTTAAAGTGGGAGGGTGGCAAGGATGTGCTTAATAAATCAA
 TTCCAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREFVYRDCVLQCEEQNCSSGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTGVLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMILLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEDEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTEVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVIQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCGGTAGAGGAAGTGGCGGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTTGCTGTCTCGTTCAGGCCCCACCCCCC
 TTCCCACCTGACCAGCCATGGGGGTGCGGTGTTTTTCGGCTGCACTTTCGTGCGTTTCGGC
 CCGGCTTCGCGCTTTCTTGATCACTGTGGCTGGGACCGCTTCGCGTTATCATCTGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCGAGATGGCCT
 ATGTTTTCTGGTCTCTCCTTCGGTATCATAGTGGTGCTTCTCTGTTATCAATATTTGGCT
 GATGCACTTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGCCCTGGTGGTTGGGAGTCACCTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCAGCC
 TCTTGTGTAAAGGACTGACTACCTGGACTGATCGCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCCACATTCCTGTCTCCTTCTCGTC
 GGCTACCCCACTACCTCCAGGGTTTTGCTTTGTCCCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTCAGCCAGTCACTGACTGGTGGGTTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGAGTGTCTGCTCTCAC
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGAGGCCGACGGCAGAGGACAGTCGGGTGAT
 GGTGATTTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACAG
 GTTGCCAAAGAAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTTCTAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTGGGTGTGATAAATACCTAAACTGCCTTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTAACCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGTCTCATGCTGGGCTCATTTGCGTCCCTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAAGTGCATGTTGGGAACTGGCATTACTGGAACATAATGGTTTAACTC
 CCTTAACCCACAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAAGTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTGCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTGTAGTTTTTAATTTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT
 ATCATTTTTCTGTGAGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGAAT
 AATAAAAAAGAAATTTGTAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA
TTTCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGATGCCTGTGA
GAGGAG

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FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGCC
TTCTACAGGAGGTGTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTCGGGCCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGCTCTGTG
CTTCTACAGGAGGTGTTCCGCTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGGAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTGTGCCCTCCTTGCCCTGTCTGGAGGCTGTCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCCGT
 CCTTGTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATAACTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT
 CAACGCTCTCCTCTCATTTGCCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCTTGTGCCCGGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCT**TGA**GTCTAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAAGTCTCCAGGGCGGGGTGCGTCTCAATCTCCCTGGGGCACTTTCTAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAACAAAAA

FIGURE 226

MATARPPMWWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYT NLCKFTKWIQETIQANS

ATGTCACACGACCGG1GGAAGACCATGGGCGCGCTGCCCACTTGAGGAACGGCCGCGGCA
CAAGCCGACGAGCCGCGAGCTCGGGCTACGTGTCTGACCGCTGCTGCTGCCCTGGCTGTGC
TCTGGCTGTAGCTGTACACCGGTGCGCGGCTGCTGCTGACCGGACGCGCCGCGGACG
GCGGCCCAACCTCTGTGCAGCATGTGGGGGCGGACGAGCAACAGCGCCCTGGCTACTGTGGA
AAGGGCGAGACGCTGCGACATGTGGGGGCGGACCTCTATGACCCGCGCTGCCCGACCTCACCAGCA
CGCTGTACGCTGTGCGGAGCGCCCGGCTCTGCTGCTGCGGCGCTGACAGACGACCAAGGCC
CGGCTGCTGTGGGGGACCGAGGACGAGGCTGCTGCACACGCTGGCCGACACGAGCTGCC
CGGCTGCTGTGGCGAGCCTCAGAGCTGCAGAGGAGTGTGACATGGGGCTGCGGAAGGGGACTG
CGACGCTGGCCGAGGCTCAGCGCTCAGAGTAGAGACGGGCGGCTCATCCAGCTTCTCT
TCTGAGAGCGAGGGCCACATGGCTCACTTGTGAACTCCGTACGCACATCTCGATGGCTCT
CGACAGGAGACGGGGGCTGGGCCGCCCGCAACAGGCCGACCTCAGAGAGCGGCTGCCCG
GGGAGACCGCGCCGGGGCTGTGCCACTGGCTCCCGCGCGGAGACTGTCTGGAAGCTCTC
CTAAGCGGACAGGACGAGGACGATGGCTCTACTCTGTCTTTCCACCCCACTACCCCGCGGCTCT
CCAGTGTACTGTGCATGCGCAGCAGCAGCGCGCGGCTGGACGCTGTTTACGCGCCGGGAGG
ACGGCTCCGTGAACCTTTCCGGGGCTGGGACGCGTACGACAGCGGCTTTGGACGAGCTCACG
GGGAGCACTGGCTGAGGCTCAAGAGGATCCAGCGCTGACACACAGGCTGCCTACGAGCT
GCAGCTGGACCTGGAGACTTTGAGAAATGCACGGCCTTATGCCCGCTACGGGAGCTCTCGGCG
TGGGCTGTCTTCGCGGACCTTGAGGAAGACGGGTACCCGCTACCGTGGCTGACTAATTC
GGCATTCCAGGCACTCCCTCTGAAGCACAGCGGATGAGTTTACCACCAAGAGCGCTGTA
CAGCGACAACTCAGAGAACAACCTGTGCCCGCTTACCGCGGCTGCCCTGGTGGTAGCCGAACT
GCCACAGTCCCAACTCTAATGGCGAGTACCTCGCGGCTGCGCAGCGCTCTATTCGCGACGGG
GTGAGATGTCTCTCTGAGCGGCTGGCACTACTCACTCAAGTTCCTGAGATGAAGATCCG
CGCGGTGCGGGAGAGGACCGT**TAGAT**CTGGTGACCTTGTCTCTTGCCCTGCTGTGCTCTTCGC
CCCATCCCGACCCCACTCACTCTTTCTGTGAATGTCTTCCACCCACTGTGTGCTTGGCGGAG
CCACTCTCCAGTAGGAGAGGGGCGGGGCCATCCCTGACACGAGCTCCTCGGCCCGGTGAAGT
CACACATCGCCTTCTCGCGCTCCCCAACCCCTCACTTTGGCAGCTACTGATCTCTTGCTCT
TGCTGATGGGGGCTGGCAACCTTGACAGCCCAACTCTGCTTGCCTCCGCCACTGTGATCTCCGG
TGCTGTTTGGCGTCCCTGCGAGGATGGTGGAGTGTGCGCCAGGACCCCTGTGCCCTGCC
GGCCAAATATCCGGCATTTATGGGACAGAGAGCAGGGGGCAGACAGCAACCCCTGAGTCTCT
CTAGACAGTCTGTGGGAATCTGCAAGTCTCTTGAGTCAAGTCTGAGGCCAGTATCTCTCAG
CCCTCCCAATGCCAACCCCAACCCGCTTCCCTGGTGCGGAGAGAACCACCTCTCCCTCCAA
GGGCTCAGCCTGGCTGTGGGCTGGTGCGGCCATCTCCAGGCGCCTGAGTCAAGTATGGG
GAGCTGTCTGCCTTTGGGAGCCGACGCTCCAAGGCTGAGACAGTCTCCTCGAGGCCACAACA
CTGTGCGCCGGCAGGCTGGGGTGTGAGCTCTTACTTACCTGCTGTGGCTGAGTCAAGTCTCT
TCTCAAAATGAGGCCCAACCCATCCCCACCCAGCAGTCCCGGCTGCTGCTGCTGAGCAG
CGGGGCTGCCATCCCACTTTCTCGCGCTCTGGAAGTGGGGGCTGCTGCTGCTGCTGAGCAG
GGACTCGCTAATGGGAAGCTCTGTGCTGCTGCGGCTGAGGCTGAGGCTGCTGCTGAGCAG
GGCTTGACACCCGCCACAACCTCTCCAGGGCTCCAGGGCTTCCAGGCTTCCAGGCTCCAGGAG
GCTTGGGGGTGATCACTCTCCCTGAGTGGCTGTCTCATGAGGAGCCCAACCTCTGCC
ACACTCACCGGGCAATGGGCTGGGGGATGGGGACAGCAGGACACCCACTGGACA
CTTTCTGTGTGAATCTCCCAACCCAGCAGCTGTCACTCCCACTCTTGTGTGCACACA
TTCAGAGTGTGACCCGACGCTCCAGGCTCCAGGACAGGCCAAGGGCAGGGCTGGAGCGGG
TCTTCAGCTGTCTCTCAGCGCCCTGGACCCGCTGCGTTAGCTCAGGCCCGAGTGTGACGG
CGGCTTTTCAAGCGCTCTGTATGGGGCTCCGAAGGGCTGGAGTCAAGCTTGGGAGCT
GCTTAGCAGCTCTCTCTCGGACGAGGGAGGGAGGGTCTCTCTCAAAGGACCAACCGATGCA
GGTGCCTAGGGGGTGTGGGGTTCGCTTCTCTCTTCCCTCCCACTGAAGTTTGTGCTTAA
ACAATAAATTTGACTTGGCACAACCTGGGGTGTGGGAGAGGCCGTGTGACCTGGCTCT
TGTCCTAGTGGCCACAGGTCATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRFPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQQGRLIQLL
SESQGHMAHLVNSVSDILDALQDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

GCAGTCAGAGACTTCCCTGCCCCCTCGTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
TGCTTCCCTGAAGTAGCTCACAGTAGCCCCGGCGGCCAGGGCAATCCGACCACATTTACTCT
CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
ATGGGGACACCACCATTAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTTGCTGAC
TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACC
AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
TGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
GACTGTAATATTTCTGCCTTAGTGAAAACCTCTACCATTGCTGAAGATAACAAACAAGAAGA
CCTGGAATTTGCCGCGCTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTTT
TGCGCCCTGACAGTGGCAGGGCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
TTCATATTTATAATAGATGTCCAGCGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
GATGATCTTCTCAAAGGACTGCAAGAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
TGGTGGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCC
CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTCTCTGTG
TTTCTGTTCAGGATACCAGCATTCTGAGCTTGGGTTTATGCAGTATTTAACAGTACA
AGAAGTCTTATTTACATGCCACCAACCACTCAGAAACCCATAATGTCATCTGCCTTCTTG
GCTTAGAGATAACTTTTAGCTCTCTTCTTCTCAATGTCTAATATCACTCCCTGTTTTCAT
GTCTTCTTACACTTGGTGGAATAAGAACTTTTGAAGTAGAGGAAATACATTGAGGTAAC
ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACC
AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGATGTCACTTGATATGAG
AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTGTGTCCTTAAAGACTCTGATAATTG
TCTCCCTCCATAGGAATTTCTCCAGAGAGAAATATATCCCATCTCCGTTTCATATCAG
AATACCGTCCCCGATATTTCCCTCAGGAAAGTAAAGACCAGAAAAAGTGAGCCTCTTCA
TTCGACCTGTGAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG
GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRSDRCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

CCGAGCGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGGGCGCGGCT
CGGGGAATTCGGCTCGGGCGCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCGCGCGGGG
CCGAGGCCCTCCGGAATCCGCCCTCCCGGTCGCCGCCCTCGAGAGACTCTTGGTGCT
CTGGGGGTTCTCGCGGGGCGGGGACCGCGGTCGCGGGCAG**ATG**CGGGCACTCGCTGCTGCT
TCTGGTGCTCGCGCCCGCAGGGCGGCTGCGCGTGGGCACTCCCTGGGCTTCACTCGACT
GCTCAGCGTCACTGGGTGGAGGAGCCGTGCTGGCCCGCGGCCCACTCGGTGCAGCCGGAGCG
AGCTGCGCGCGCGCGGCAACACCAAGCGCGCGCGCGGCCCACTCGGTGCAGCCGGAGCG
GAGGCGGAGAAGCCGGGGCGCGGAGCGCGCGGGGAGAATTGGGAGCGCGCGCTTGTGCC
CTACCACTCGTACAGACGGCGCGCGCGCGCAAAAGGCGCTGACGAGCCGCTACATCAGC
CGGAGCTGGGCACTCAGGCAGAGGCTGCTGGTGGCGGTGCTACTCTCAGAACAGCTGCC
ACGCTGGGGCTGGGCTGTAACCGACAGCTGGGGCAGCGGCTGGAGCGTGTGGTGTCTTCAG
GGCGCGACGGGGCGCGGGCCCACTGCGATGCGATGGCATGGTGGTGGACGTGGCGAGGAGCGAC
CCATTGGACACCTGCACCTGGCGCTGCGGCACCTGCTGGAGACGACGGCGAGCACTTTCAG
TGGTTCCTTCTGGTGGCTGACACCACTACACCGAGGCGACGCGCTGCGACCGCTTAATGG
CCACTCAGCTGGGCTTCGCGCGCCCACTGTACTGGGCGGGCCCGAGGACTTCATCGCG
GAGAGCGCAACCCCGCGCGCTACTGCGACCGAGGAGCTTGGGGTGCTGCTGCGCATGCTG
CTGCAACAACCTCGGCCCACTGGAAGCTGCGCAACAGCATGTCAGTGGCGCCCTGA
CGAGTGGCTTGGTTCGTCGATCTGTCAGTGCACCGGGTGGGCTGCACTGGTGACCCAGG
GGGTGCACIATAGGCATCTGGAGCTGAGCCCTGGGAGGCCATGACGAGGAGGGGACCTTAC
TTCGGAAGTGGCTGACAGCCCACTTGTGCTGACCTGTGCACATGTACCAAGTGCACGA
AGCTTTCGCGCGAGCTGAACCTGGAACGCACTACAGAGATCCAGAGATTCAGTGGGAGA
TCCAGAATACAGGCATCTGGCGGTGATGGGGACCGGGCAGCTGCTTGGCCGTCGGGTATT
CCAGACCACTCCCGCGCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCAGGACA
GCACGCTTTCTCTCGCGCGATGGCTACCCGCTGCCACTGCGTGCGGTGGGGTGACCGGCTG
ATGTGGCCGATGCTTGTGGGACAGCTGTAGAGAGCTGAACCCGCTACCAACCGGCTCGT
CGGCTCGACAGGACGACGCTGTGTAATGGCTACCGACGCTTTGATCGGCGCGGGTATGGA
ATACACGCTGGACTTGCAGCTGGAGCACTGACCCCGCAGGAGGCGCGCGGCCCTCACTC
GCGGAGTGCAGCTGCTCGCGCGCTGAGCGGCTGGAGATCTTGCCTGTGCCCTATGTCACT
GAGGCTCGACGCTCACTGTGCTGCTCCTCTAGCTGCGGCTGAGCTGACCTGGCCCTGG
CTTCTGTAGGCGTTTGGCACTGCAGCACTGGAGCCTGGTGATGCTGCGCGACGCTGACC
TGCTGCTGATGTATGAGCGCGCGACGCCGCGCGGTGGCCATGCAGATGTCTTCGCACT
GTCAAGGCCCACTGTGGCAGAGCTGGAGCGCGTTTTCGCGGTGCGGGGTGCATGGCTCAG
TGTGCAGACAGCGCGCACTCACCATTGCGCTCATGATCTACTCTCAGAGAAGCACCGCG
TGGACACACTGTTCCTGTGTCGCGGGCGCAGACAGCGGTCTCAGCGCTGACTTCTGAAACCG
TCCGCGATGCATGCATCTCCGCTGGCAGGCTTCTTTCACATGCATTTCAGAGCTTCCA
CCCAGGTGTGGCCCCACCAAGGGGCTGGGCCCGCAGAGCTGGGCGCTGACATGGCCGT
TGTGATCGCCAGGCACGCGAGGCGCTGCTTCTACAATCCGATACGTGGCGAGCCCTGGG
CGCTTGGCGCGAGCTCGAAGAACAGAGGAGCTGCTGGAGAGCTGGATGTGTACGAGCT
GTTCTCTCACTTCTCCAGTGTGCATGTGCTGCGGGCGGTGGAGCGCGGCTGCTGCAGGCT
ACCGGCGCGAGAGCTGCAGCGCGAGGCTCAGTAGGACCATGTACCACCGCTGCTCCAGAGC
GTGCTTGTAGGGCGCTCGGCTCCCGAAGCCAGCTGGCCATGCTACTTTTGAACAGGAGCGGG
CAACAGCAC**TGA**CGCCACCTCTGTCCCGTGGGCGGTGCATGGCCACACCCCACTTCT
CTCCCCAAACAGAGGCACCTTCTGCGCTCTGTGGGAGAGGCTGGCCGTAGCCAGACCC
AAGCTGGCCCACTGGTCCCTCTCTGCTGCTTGTGGTCCCTGGGCTGTGGAACAGCACTGGG
GGAGCTGCCCGCAGGCCACCACTTCTACTCCAAACCCAGTTCCTTGGCCCTGTGAGCT
GCTGATTTCGGGCTGTGGCTCCACGTAATTTATTCAGTACAGTCTGCTCAGCCGAGCCCTGC
CTCTGGGCGCTGGGGGCTGGGCTGTAGAAGAGTTGTGGGAAGGAGGAGCTGAGGAGGGG
GCATCTCCCAACTTCTCCCTTTTGGACCTTCGCCAAGCTCCCTGCCTTTATATAACTGGCCA
AGTGTGGAAGAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGF TLLSVTWVEEPCGPGPPQPGDSELP PRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQA AKKAVTRYISTELGIRQLLVAVL
TSQTTLPTLGAVNRTLGHRLERVVLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGDDEFDWFFLVPDTTYTEAHGLARLTGHL SLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGR CILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALT AHPVRDPVHMYQLHKAFARA ELERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAA PSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALQRYRAQTC SARLS EDL
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGGAACCAAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCGCCCCCTGAGACCCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAATGCTTCGACCCGAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRGLPAAVRWESSFSRTVVAPSAVAGKRPPEPTTFWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGCTGGGCTGTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCCAGAACCAGCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGCTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CGGCTTGCTCTGCTCGTCTGTGCTCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCCAACGCGACAGCCTGCGGGAGGAACTTGTCATACCCCGCTGCCTTCCGGGG
 AGCTAGCCGGCACATTCAGTTCCGACGCGCTGGGATTTCGAGCTTCAGCGGGAAGGAGTG
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCATTACACAAGGCTTTTGGAGACCCGATCTGCGGGCCACCTTCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCCGGGAGGTGGTCTGCAACGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACACAGCTACCACTCCCAAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCACTGTATTGTGATGCCTTC
 ATCACGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGATGTTCTCCCGAACCTCACGGA
 GCCTTGCCCTTGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTTACAACACAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCACTCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGAAAGAGACCCCGAGAGATGAGGCCCCCCAGTGCCTTCTGTC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCTGGTATCTGGG
 GCTGTATGTGCACACCTTCAACATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACAGCCTGCCAGGACCGGCTGCAACCCCACTCCTGGAGATGCTGATTGAGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CAGCCAGATCTTAACCATGGCTTCTATGTACGCCATCTGCTCCTCAGCGCCCTTGTGCCCA
 GCATGTTAGCAGCAAGCCAGTGGACTGGGAAGAGATCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTTAACACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGGCTTACACGCTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGCCCAAGCGGCTGGCCAACTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**CGA**TT
 CTGCGCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAGTGCCCTGGACCAAGGTGAGGGC
 CTACAGCTGTGTTTCCAGTACAGGAGCCAGGACCAATGTGGCATTTGAATTTGAATTAA
 CTTAGAAATTCATTTCTCACCTGTAGTGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCCGTGGCTGCTGATTGGACAGCACAGAAAAGATTCCATACCCACAGAAAGGTC
 GGCTGGCAGCACTGGCCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCAGTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLPGGWCIAPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSIWELRQTLSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPEAEAPPVFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPDPFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAAC**ATG**GGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACGTGTGGCTTCAAGTGTGTGATTCCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAA**TGA**TGCTGGGTCCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCTTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMSLVLTVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYEPGWAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTTGGCCGAGTGGCTCATTGTTAAGACAAAGGTTGTCACCTTCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCCTGCCTGTGGAGATGAGGACCTTGAGCCAAAGG
 CGTCCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTCGCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACAATTAAAGAAAGGTC
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACCGAGGCCAAAGCGGCAACCAAGCAGCAAGACGCTCATTCCTCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGGCACCCACCCCTTGCCTCTTCCAG
 AGCCCCACGACGCAAGAAACCAAGAGCTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAATAGGAGGCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGAAGTGGGACCGCCTGGAACACTTTGCACCACC
 CTTTGCTTACATGGAGCTCAACTACTCCTTGCTGTCAGAAAGCTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGATCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTACCGCCTTCTCCCTGACCCAGTCACTCCTATATTTGGGCAAT
 CGGGGTTTCAAGAACGTGCCCTCTGGGAAGGACGTCCGCTACTTGCACTTCTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGTGTTCAAGCACAGACCCAGGAAGCTTTTCGGGAAGCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGCTTAAGACCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACCAGGCTCCCTGGTC
 CCGGAACCTGCCAAAGCCAAAGAACTGA**CG**CGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCTTCAAGGAGTCCAAAGGGAACACTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTTCTGAAGTCTTTCAGTACATTGCTGTAGGTCCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGACTCTG
 GTTGAATTCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACCTCACTAC
 AGATTGCTAGAAAGACCTTTCTAGGAGTTATCTGATTCAGAAAGGCTATACATTTGCCCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAGGCCAAATAAATTTTCTACAGTGAACAAAAA

FIGURE 242

MRSC LWRCRHLSQGVQWSLLLVFFLFALPSFIKEPQT KPSRHQRTE NIKERSLQSLAKP
 KSQAPTRARRTTIYAE PAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVT TAVI PPKEKKPQATPPPAPFQSP TTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPF GFMELNYSLVQKV VTRFPFPVQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQQEIDSHDYVFR LSGALIKGYEQDVGTRTSFYGF TAFSLTQSL LILGNRGFKNVP
 LGKDVRYLHFLEGRDYE WLEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLL LHPDFL
 RYMKNRFLRSKTL DGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKR LHDEGIIRLYQRPGGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

244/330

FIGURE 244

MRGPGHPLLLGLLLVLGFSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKH FHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

100
90
80
70
60
50
40
30
20
10
0

FIGURE 245

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGCTCCTGCGGTCCCTTCTCTGGGAGG
CCCGACCCCGCGCGCGCCAGCCCCACCA**ATG**CCACCCGCGGGGCTCCGCCGGCCGCGCGG
CTCACCGBAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGACGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCAAGGGAAGTGAACAGGAGCTGAACTAGA
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVGLAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYFYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCCAGCTAGGTAGAGCAAGAAG**ATGGT**GTTTCTGCCCTCAAATGGTCCCTTGCAACCATG
 TCATTTCCTACTTTCTCTACTGTGGCTCTCTTAACTGTGTCCACTCTTCACTGGTGTCCAGAG
 CTACTGAAGCATCTCCCAACGCTAGTAGTGGGACACCAATTTCCCTGGAAATAAAATACGACTTC
 CTGAGTACGCTACCCAGTTCATTATGATCTTTGATCCATGCAAACTTTACCACGGCTGACC
 TTCTGGGGAAACCAAGAAAGTGAATAACACGCCAGTCAAGCCACCAAGCACCATCTCTGCA
 TAGTCAACCACTGCGAGATATCTAGGGCCACCCCTCAGGAGCAAAATTGCATGCTGGCTCCCGAG
 AAGAACCCTGCGAGGTCTGGAACCCCTCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 CCCCCTCTTGTGGGCTCCCGTACACAGTTGTCTATTCTCATGCTGGCAATCTTTGGAGAGC
 TTTCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGAAGGATACCTAGCAT
 CAACACAATTTGAACCCACTGCGAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAGCGAAGTTTCTCAATCAAATTAGAAGAGAGCGCAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTTGTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA
 AGATAGCACCTATCTGTGGTGGCTTTCATCTTTAGATTTTGAGTCTGTGAGCAAGATAACC
 AAGAGTGGAGTCAAGGTTTCTGTTTATCTGTGGCAGACAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGCTCTCTCTGAATTTTATGAGGATTATTCAGCATACCGTATCTCCCC
 TACCCAAACAGATCTTGTGCTATCTCCGACTTTAGTCTGGTGTATGGAAAACCTGGGGGA
 CTGACACATATAGAGAATCTGCTCTGTTGTTGATGCAAGAAAGTCTTCTGCATCAAGTGA
 GCTTGGCATCAGCTGACTGTGGCCATGAACCTGGCCACCGAGTGTCTTGGAAACCTGGTCA
 CTATGGAAATCTGGGAATCTGCTTTGGCTAAATGAAGGATTGGCAAAATTTATGGAGTTTGTG
 TCTGTGAGTGTACCAATCTGAACTGGAAGTATTTCTTTGGCAAAATGTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTGTACACCTGTGGAAAATCCTGT
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTGTATTCTGAAATG
 CTAAGGGAGTATCTTACCGCTGACGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAAATACAAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTGGCCCTACAG
 ATGGTGTAAAAGGATGGATGGCTTTTGCTCTAGAAGTCAACATTTATCTTCACTCCACAT
 TGGCATCAGGAAGGGGTGATGTGAAAACCATGATGAACATTTGGACCTTGAAGAGGGGTTT
 TCCCTATTAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTAGCGGCGCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACC
 AGCAAAATCAACATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCC
 AGAGAGTGGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTACG
 AGGATAGTGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACAGCAGCTCAGCAGT
 AATGATCGGGCAAGTCTCATTAACAATGCATTTACAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGAAGCCCTGGATTATCCCTGTACTGAAACATGAAACTGAAATATTGCCCGTGTGATG
 AAGCTTTGAATGAATGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTCAGGCGCTTCTCATCAGGCTGCTAAGGAGCTCATTGATAAGCAGACATG
 GACAGACAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAATCACTCTCCCTGCTGTG
 TGCACAACTATCAGCGCTGCGTACAGAGGCGCAAGGCTATTTTCAGAAAGTGGGAAGGAATCC
 AATGGAAACTTGAAGCTGCTCTGTCAGCTGACCTTGGCAGTGTTTGCTGTGGGGCGCCAGAG
 CACAGAAGGCTGGGATTTTCTTTATAGTAATATCAGTTTCTTTGTCCAGTACTGAGAAAA
 CGCAAAATGAAATTTGCCCTCTGCAGAACCCAAATAAGGAAAAGCTTCAATGGCTCATAGAT
 GAAAGCTTTAAGGGAGATAAAAATAAAACCTCAGGAGTTTCCACAAATCTTTACACTCATTTG
 CAGGAACCCAGTAGGATACCACTGGCCTGGCAATTTCTGAGGAAAACCTGGAACAACTGTG
 TACAAAAGTTTGAACCTGGCTCATCTTCCATAGCCACATGGTAATGGGTACACAAATCAA
 TTTCTCCACAAGAACCGCTTGAAGAGGTAAAAGGATCTTCAAGCTATGTGAACGTATGTAAA
 TTTCTCAGCTCCGTTGTGTCCAACAGACAATGAAACCATTGAGGAAAACATCGGTGGATGG
 ATAGAATTTTGTAAAAATCAGAGTGTGGCTGCAAGTGAAGAGCTTGAACGTATGT**AAAAA**
 TTCTCCCTTGTCCCGGTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA
 ACTAGAGATGCTGTTTGGCTCCAACTGGAGATCTTTTTCCCTTCACTCATCTTTTGA
 CTATCCCTGTGAAAAGAAATAGCTGTAGTTTTCATGAATGGGCTTTTTCATGAATGGGGT
 TCGCTACCATGTGTTTGTTCATCACAGGTGTGGCCCTGCAACGTAAACCAAGCTGTGGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEELQVLVE
 HPPQEQIALLAPEFLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELAHQWFGNLVTMEWWNDL
 WLNNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTFVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYIIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKCRDMNEVETQFKAFLIRLLRDLIDKQWTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTESKQIEFALC
 RTQNKEKLQWLLDESFGDKIKTQEFQILTLIGRNPVGYPLAWQFLRKNWNKLQKQFELGS
 SSIAHVMVGTQNFSTRTRLEEVKGGFFSSLKENGSQLRCVQQTETIETIENIGWMDKNFQKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCACCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCACAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTC
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTGCGTGGCCCCAACCTTCAGCTTCTTGTGTAACACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCTAACTCTATTACCCCCACGATTCTTACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTATATCTACTACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

FIGURE 250

MSAVLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTGWVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
 CAGGATGAGGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGTCTGT
 GGAAAAATTTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTTGCAGGGCCGCGGGGACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTTCATGTGTGAGTTTGACAA
 GAGAACATGTTGAGCCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCTTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAAATGGCCTATGCTTAAGAGGAAAAATG
 AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCCTTTGTCCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAA

FIGURE 252

MRGNIALVGVLLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGDMDKGQKGSVGRHGKIGFIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM



FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCCTGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTTCGGCCC
 CTTTCATCCCAATCAGCTTGATCCACAGGAAAGTCTTCCTGGGAACAGAGGAGCAGAGACC
 TTTATAAGACTCTCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGA¹TCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTTAGAGTTCCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPRL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCTGTGCCTGCTGTGCC
 CGCGTGTGCGCCGTGTACCGCTGTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTGGTGGTGTATCCCCCTGGGGC
 TGCTGTTCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCCGGGGTGGGGC
 CTGGGCCACCGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCGAGCCAGTGCCTGTGATGG
 CTGGCTCAGGCTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTGTT
 TTGAGACAGGCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCCGAGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGT
 CTAGGATTATAGGCATGAGTCAACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGGAAGGAGCTAACGCTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGT
 GATTGTGATGGTGTTCCAGGTGTGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAACCTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCCATCCGTCACTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAACATGGTAAAGCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

FIGURE 256

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLVFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCCCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTGCGTATGCTG

258/330

FIGURE 258

MSGGLPLVLLLTLLGSSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHVVNT

258/330

FIGURE 259

AATTGTATCTGTGAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACATAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTAGCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATAGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCTCTGACGCTTTTCTGCCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGCTTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAGCAACGAGGGGCATACATTCAAGAATTTCAAGAGTTCTCAAAAAATATA
 TCTGTCTGCTGGGAAGATGTCAGACCTACACAAGTGAGTACACAAGATGCAGTGGGTAACTT
 GGCACGTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACATACCTTTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTATTATAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTCTATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAACTCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTCTATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGACCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCACCCATAGCCATTGTTTCTCA
 CAAAGATTGAGCCGGGCACTGGGAGTGGAGCATTGATGGATACCCCATGCGAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGCACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAAACCCAGAGAT
 AAGCAGCTCTATGCCTTGAATGAAGGAAACAGATCATTTACAAACTCCAGACAAAGAGATCA
 GCTGCCCTCTGAAGTAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCCTCTTCCCCAAATGTCACTGCCTTAGGCTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAA
 CCTCCTGGCTCTCAGGATGACCACATTCTGATCAGCCTACTCTAAGCCTTTGTGTTTTACT
 GCTCCCCAGCAATTAATGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCTTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAAATCTATTAAATATTCTTT
 CTTTTCTTTTTTTTTTTTTGAGACAAGGCTCACTATGTTGCCAGGCTGGTCTCAAATCC
 AGAGCTCAAGAGATCCTCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACTGGCTTAAATATCTATTCTATTAGGTTTAACTCTATTTCCTTAGCCCTGTCT
 CTTTCCATAGCTTGGTAGATGTAATAATAAAGTGAAAAATATTAACATTTGAATATGCCTTT
 CCAGGTGTGGAGTGTGTCACATCATTTGAATTTCTGTTTCACTTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAAATACAAAGTGAAGATACAGC
 TAGAAAAATCTACAAATCCCATAGTTTTTCCATTGCCAAGGAAGCATCAAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCACTGTTTCAAGCCTTAAAAATATAGTCTGTCCC
 TTTAGCCAGTTTTTCATGCTGCACAAGACCTTTCAATAGGCCCTTCAAAATGATAATCTCTCC
 AGAAAAACAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTGTCTGTCTGCTCTGTCT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVFLAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLNASCNMLMGIKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAACATGAGAGCTCTCGCAGA
TGTCGGAGCTCATGTTGGGCTGTCTGGTGTGCTTGGGCTGCTGCCCTGATGGCGACGGCGCG
GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGACGGCGCGCCCGGCTGCCAAAAGAC
AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAAAACAATATCAGCGGATTC
GGAAGGAGAGCTCTCAACAACAACCTTACCCAGCCGCTCTGGCTGCAGCTTGAAGAGC
CACAGCGGGAACATATCTTGATGCACTTTAGACGAATGGCAAATACCTGGCTACCTGTGC
AGATGATCGCACCATCCGCATCTGGAGCACCAGAAGCATTTCTCGAGCGAGAGACCCGACGC
TGAGACGCAACGTGGAGCTGGACACGCCACCCCTGGTGGCTTACGCCCTGACTCGAGACC
TTCACTGCTGCTGGTGGCCAAACGGGACACCTCGTGCTTCAAGATGACCAAGCGGGAGGA
TGGGGGCTACACCTTACAGACCCACGAGGAGGATCTCCCTAAAAGCCACAGGCGCCTGTCA
TCGACATTTGGCATTTCAACACAGGGAAGTTTATCATGACTGCTCCAGTACACCATCTCTC
CTCATCTGGAGCTGAAGGGTCAAGTGCTGTCTACCATCAACCAACAGCATGAACAACAC
ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTFGTTGGCTTCACCCAAGATGTGA
AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGAGTTCAGGAGGCTGTGCGAGCTCTCGAA
CTAAAGGCGACTCCGCGGCTGTGCACTCGTTTGGCTTTTCCAACGACTCACGGAGGATGCG
TTCTGTCTCCAAGTAGGTGATCATGGAAATCTGGGGACAGGATGTGAATACAGAAGAGAC
AGGACCCCTAATTGCTGAAGACAGCGCGCTTTGAAGACGCGCGGTTGCGCGCGCTGCCGC
CTGGCCCTCTCCCCACGCCACCCAGGTCTTTGGCTTTGGCCAGTGGCAGTAGTATTCTCTTA
CAATACCCGGCGGGCGGAGAAAGGAGAGTGCTTTGAGCGGGCTCCATGGCAGGTGATCGGCCA
ACTTGTCTTTGACATCATGGCGCTTCTTGCCCTCTGTGGGACCGCGGCGCTGTGCGGCTG
TTTCAACAACACTCTGGCCACCCGAGCCATGGTGGAGGAGATCGAGGCGCCCTGAAAGCGGGC
CTCCAACGAGAGACACCCGACGAGGCTCGACAGCAGCTGACCCAGCCCCAAAGAGCCCTGA
AGAGCTGGGTGGCCTGAAGAAGTGAATCTTGGAGGGCGCGCGCAGGAGTTAGGAGGAG
GGATCTGGCTCTCATGGCACTGTGCCATCTTTCTCTCCAGGTGGAAGCGCTTTCAGAAGG
AGTCTCTGGTTTCTTCTAGCTGGTGGCCCTGCTTCTTCCCATTTGAACTACTCTTGCTACTT
AGGCTCTCTCTCTTGTGCTGGCTGTACTCTCCCTGACTAGTGGCCAAGGTGCTTTTCTCT
CTCCAGGCGGAGGTGGTGGATCTGTGCCCACTGGCACTGAGGAGAAATGTTAGAGAGAG
AGGAGAGAGAGAGAGAATGTGATTTTGGCCCTGTGGCAGCAGTCTCTACACCAAGAAG
TTTGTAAATGTTCCAGAACACCTAGAGAACCTGAGTACTAAGCAGCAGCTTTTGAAGGA
TGGGAGACTGGGATAGCTTCCATCAGCAAGCTGTGTTTCATCAAAAAGACTAAGGGATT
TCTCTCTGGCCCTCAGTTCTATTGTAGATGGAGAATACTCTCTGTGACTCTGTCGCA
AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
AGTACTATTGTCCAATGTCTGAAGAGTGGTAAAGGTGGAACAGGTGCTTTGAAGACAAA
TTAGAACAACCTTCTGGGAAGGCAAGTTTCTGGGACTGATCATACATTTATATGCT
TGGGACTTCTCTCTCGGAGATGATATCTGTTTAAAGGAGACCTCTTTGAGTTCATCAAG
TTCATCAGATATTTGAGTGCCCACTGTGCCCAATAAATATGAGCTGGGATTTAAAAAA
AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFIWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLLKRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAAGTGTGTCTGACTGTGTGATCACAGGGGCCCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCAGGAGTGCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGTCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGCCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCTCCCTCCCGAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCAGGTCTGGCCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTGATGCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTCCATTAAAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFDPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAGGGAGGCACTTGAGAAATGCTCTTTC
 CTCCAGGACCCAAGTTTCTTCCCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGCATTCTTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGATT
 GTTTCCTCTCGTGTCCCTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACCTTGAGGTGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAACTCACTTGAACCTGGGAGGTGGAGGTGCGGTGAGCTGAGATCA
 CACCACTGTATTCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLKEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEI FLDEKKKFYGPQRRKMMFMGFIRLGVVYNFFRAWNGGFSGNLEGEF ILGGVFV
VGSGKQGILHEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK



FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
GGCCAGGTGCCCCGTGCGAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACC CGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCCTGCCGTTCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

FIGURE 273

GCCAGGAATAACTAGAGAGGAACAAATGGGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCCCTGCTGCACCAAGTCAAATACCTCCCTTCATTAAAGCTGAATAATAATGGGCTTTGAGGATA
 TTGTCATTTTATAGATTCCTAGTGTGCCAGAGAATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAATTCCTGAGAATTTGGAAGGAAAACTCTCAGTACAAAAGGCCAAAAACATG
 AAAACCATAAACATGCTGATGTTATAGTTGCCACCACCTACACTCCCGAGTAGAGATGAACCA
 TACACCAGGCGATTTCAGAGAAATGSGAGAGAAAGCGAATACATCTACTCTACCCCTGACCT
 TCTACTTTGGAAAAAAACAAAATCAATATGCACCACCAGGCAAACTGTTTGTCCATGAGTGGG
 TCCACTCCGGTGGGGAGTGTTTGATCAGTACAAATGAAGATCAGCCTTTCTACCGTGTCTAAG
 TCAAAAAAATCGAAGAACCAAGGTGTTCCCGCAGGTATCTCTGGTAGAAAATAGAGTTTATAA
 GTGTCAAGGAGGCCAGCTGCTCTTAGTAGAGCATGCAGAATTGATTTCTACACAAAACCTGTATG
 GAAAAGATTGTCAATTCCTTCTGATAAAGTACAAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCCTGTGTTGAATTTGTACGAAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAAACATAAAGTCAATTTAGAACTACATGGGAGGTGATTAGCAATTCCTGAGGATT
 TTAAAAACACCATACCATGTGTGACACACCTCTCCACTGTCTTCTCATTTGCTGAAGATC
 AGTCAAGAATTTGTGCTTTAGTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCT
 AAATCGAATGAATCAGCAGCAAAAACTTTCCCTGCTGCAGACTGTTGAAAATGGATCCTGGG
 TGGGGATGGTTCAGCTTTGATAGTACTGCCACTATTGTAATAAGCTAATCCAAATAAAAAAGC
 AGTGTATGAAGAAACACATCTATGGCAGGATTACCTACATATCCCTGGGAGGAACCTTCCAT
 CTGCTCTGGAATTAATAATGCAATTTCCAGTGAATGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGGCTGCTGACTGATGGGGAGGATAACACTCTGCAAGTCTCTGTATTTGATGAAGTG
 AAAACAAAGTGGGCGCATTTGTCATTTTATTTGCTTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGATTGAGCAAGATAACAGGAGGAGTCAATTTTATGTTTTCAGATGAAGCTCAGAACATG
 GCCTCATTTGATGCTTTGGGGCTCTTACATCAGGAAATACATGATCTCTCCAGAAAGTCCCTT
 CAGCTCGAAAGTAAGGGATTAAACACTGAAATAGTAATGCCTGGATGAACGACACTGTCAATA
 TGATAGTACAGTGGGAAGGACACAGTTCCTTCTCATCACATGGAACAGTCTGCCCTCCAGTA
 TTTCTCTCTGGGATCCACTGGAAACAATAATGGAATAATTTCACATGGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTTCCAGCAACTGCAAAAGTGGGCATTTGGGCATACAACTTTCAAGC
 CAAAGCGAACCCAGAACATTAACATTTACAGTAACCTCTCGAGCAGCAATTTCTTGTGTC
 CTCCAATCACAGTGAATCTACAAGGATATGTACCTGTCTTTGGAGCCAATGTGACTGCTTTCAT
 GTTTACGCAGAAATCTACAGGATATGCAAGATTTTGGAACTTTTGGATAATGGTGCAGGCGCTGAT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAGTTTGGGATCATGAGGAGCAAACTGCCAGCTTAAATACGGCTCCCAT
 GAATAGAGCCGCTACATCAGGCTGGGTAGTGAACGGGGAAATGAAGCAAAACCCGCAAA
 GACCTCAATTTGATGAGTACTCAGACACCTTTGGAGGATTTGACGCCAAGCATCCGGA
 AATCACAGACCTTGTAGCCACAGTTCTAGGAGTAAGATATTTCTTACATGGACAGCACCAG
 GAGATAATTTTGTGTTGGAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTTCTT
 GATCTACAGCAAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACCAAGGA
 GGCACTCTCAGGAAGAACTTGCATTTAAACCAAGAAATATCTCAGAGAAATAATGCAACCC
 ACATATTTTATTTGCCATTAAGAGTATAGATAAAAGCAATTTGACATCAAAAGTATTTCAACATT
 GCACAAGTAACTTTGTTTATCCCTCAAGAACTCTGATGACATTCATCCTACACCTACCTCC
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTAT
 TGCTGTGATTTGGGCTGTGTTAATTTGTTAACTTTATTTAAGTACCACTTTGAACTTTA
 ACGAAGAAAATAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAACAAATGTAAGT
 AAAGGATATTTCTGAATCTTTAAATTCATCCCATGTGTGATCATAACTATAAACTAATTT
 TTAAGTCTCGGAAAAGGATACTTTGATTAATAAAAAACACTCATGGATATGTAAGAACTGT
 CACAGATTAATAATTAATAGTTTCAATTTTGTATTTTATTTGTAAGAATAAGTGAATGAC
 AAACATCTTTTTTCATAGTACCTGGTGTATATTTTGTGAACACAGTTTTCTGAAAT
 GATATTTCAATTTGCATCAAGAAATTAATCATCTATCTGAGTAGTCAAAATACAGATAAA
 GGAGAGCAAAATAAACCAACATTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

MGLFRGFVFFLLVLCLLHQNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEIQIEDMVTTASTY
LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLGRDEPYTKQFTEC
GEKGEYIHFTPDLLGKKQNEYGPPKGLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKQGGSGLSRACRIDSTTKLYGKDCQFFPDVKQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVINSSEDFKNTIPMVTPPPPVFSLLKISQIRIVCLV
LDKSGSMGGKDRLNRMQAAKHFLLTQTVENGSWFGMVHFDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGGSEVLLLTGDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSNGTDLSQLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAMKNKDVSFSPSMIVYAEILQG
YVPVLGANVTAFILESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTTAYTENGRYSKLVRHAG
GANTARLKLRPPLNRAAYIPGWVHNGEIEANPPEIDEDQTTLEDFSRTASGGFAVVSQV
PSLPLFDQYPPSQITDLDAVTHGEKIILTWAPGDNFVGVQYRIIRISASILDRDSFDD
ALQVNTTDLSPKEANSKESFAKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIP
QANPDIDTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible]

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKEFKRLILFRPFSP
MKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDLTPEQYKCMQMS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGA CTGCCATTTCATGCTGAAC TCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCC TGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCTATGA CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCTGCTTCTCTCAAGAAATTAACATTGTGTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGAATAAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAGCTATTCACGAC
 TCAAAATATTTCTAAAATATTTTCTGACAGTATAGTGATAAATGTGGTCATGTGGTATTTC
 TAGTTATGTATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGAATTT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTGTTGACCATTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVVTDPKHNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

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FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGCTCGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGT
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGTTAAAAATGCACTTTCTCCAGCTTTGCCCCGTGGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAAGACCGGGTGCTTTGGGATGGGAATCCTGAGCGGTACGA
 TGCTCCATCCTTCTCTGGAACTGCAGTTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAGACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAAACA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAGCC
 AATTTGTCTGTACATTTCTTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCTTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATTCAAAGTGTAAATGACATTTTTATTTTATGTCTC
 TCCTTAAGTATGAGACACATCTTGTCTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTCG

280/330

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIQSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

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FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTCTGCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCTTACCCTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCAGTTTTACCCTAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCCTGTGATTTT
ATCCAACTACTTACCTTGCTTACGATATCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTGTCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAA**AACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAACCTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCACTTACTCGGGAGGCTGAG
 GCAGGAAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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FIGURE 285

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
CGGGGCCGGGATGCAGCCCAGGAACCTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGCGCTCCAGCCT**TGA**ATCTGCCTGGATGGAAGTCTGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGAGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCTACACACCCCTCATTTAAAGCAGAGTCTGTCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

MPVPALCLLWALAMVTRPASAAPMGGPQLAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTEIELLGGQVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQRHLRQ
IQERLHTAALPA

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAAATGGACTTGTAAATTTGCAT
 CCTGGTGTACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAGAGGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCACGGAATCGCTATCTCCTTCCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGCTCTTCTCCCAATCAGTCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGAGCAGCAAGAGATACATATGCGAGTTTACCATCCC
 TAAAT**TAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACCTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
 TTTGTCAGCCCATACCCCTTATTTGAATTGCTCCATCTCTGGTGGGACTTGTATCTTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAGCTGAAAACCTGAATTTAAGAATGCTATCTTGGAAAATTCATACGCTCTGTGCAATT
 TTTTATTCTGCCATGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAATATCAAATTACAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSAQGK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCCAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

290/330

FIGURE 290

MKLAALLGLCVALSCSSAAAFVLVGSAPVAPVAALESAAEAGAGTLANPLGTNLNPLKLLLS
SLGIPVNHLEGSQKCVaelGPQAVGAVKALKALLGALTVFG

290/330

FIGURE 291

TGAAGGACTTTTCCAGGACCCAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAT
 CTTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCTGCTCTCCGTCTCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCTAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTCGGATTCAGCTGCTGCCAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCTTTGGCCATGACAGGGTTGATGCTGGGGGCCA
 CAGGGCCGACTGAACCCAGATCAAGAGAGGGGCTCCACTTGCAGGCCCTGAAGCCACCAAG
 CCCGGGCTCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAC
 GGGCCTCTCACAGGGGAGTTTTGCCTTCAATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTCCCAAAC
 GTTTGATGAGATTAATCTGAAACCAAAATTAATCTTGTGGATTACATCTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTTGACAAGAA
 TTTTCGTGTGATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCCAGAAACATGGAAGTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAACTCTCTCACCCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCATGCCCTCTGTGATCAAAGTGAGCCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCTCTA**TA**ATTACAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTTCTTAACAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAAATCA
 CATCTGGGTGGGACAGACAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTCTGGAATTTTTCATTAAATGTTTTGGACCATTGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCATGGATTAAGGGAGGACTACTACAAA
 GCATTAATGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVPSLLLSVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNFGFSLLRKISMRHDGNMVFSPPFGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGLLPSLFKGLRETLNRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTFFDP
VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
ALEDYLTDDLVTWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIFFSPFADLSELSA
TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLF
LGRVVPNTLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
TGTCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTCTCTGAGTCCC
GAGCCCCACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

[illegible][illegible]

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCGACCACAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTCGGGGATT
 TGTTCAATTGAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCGCGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGATCCTGCGCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGCGCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTTATCTATTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATTCT
 CTTTTTGAATAAGTATAAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAAGTAATTGAAGACGTCACTCAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACCTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACATAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

CAGCGCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCGGGAGCCGG
TCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGGACCCCTGTGGGGAGGC
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCTGGCGCTTCCGTGCTGCTGCTGGC
GCAGCTGTCAGACGCCGCCAAGAATTTGAGGATGTCAGATGTAATGTATCTGCCTCCCT
ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAAGAAGCATACTGCTACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACTGCTGAACAAGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGCTCTTTGACCGG
CATGTTGTCTCAGCTTAATTTGGGAATGTAATCAAGTGACTAGAAAGAACAGGCAGACAA
CTGGAAAGAACTGACTGGGTTTGTCTGGGTTTCATTTTAATCACTGTTGATTTCACCAACT
GTTGCTGGAAGATTCAAAACTGGAAGCAAAACTTGCTTGATTTTTTTTTCTGTAAACGTA
TAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTCTCTATTG
TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTG
TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
AACAACCTTTTTCAAGTCACTTTACTAAACAACTTTTGTAAATAGACCTTACCTTCTATTG
TCGAGTTTCATTATATTTTGAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
ACTTTTGCCTGACTGTATTAFTCTGGGTATCTGCTGTGCTGCACTTCATGGTAAACGGGAT
CTAAATAGCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
TGCAATAAAGAAATTTTATTTTAAAGCCCAAGCTCCCTGGATTGATAATATATACATTTG
TCAGCATTTCCGCTCGTGGTTGAGAGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
AGGGCTGGGGTGTGGGTGCTCTTCTGAAGGTCATAACCATTATTGGATAACTGGCTTTTT
TCTTCTCATGTCTCTCTTTGGAATGTAAACAATAAAAAATAATTTTTGAAACATCAA

300/330

FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSVTIKVTIIIIYLSILG
LLLLYMVYLT
LVEPILKRRLFQHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYA
QQRWKLQVQEQ
RKSVFDRHVVLS

2011-03-06

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCAATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACCTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACACTAACAAAGGCAGAAGTACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

MAYSTVQRVALASGLVLALLLLPKAFLSRGKRQEPPTPEGKLGFRPPMMHHHQAPSDGQT
 PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILI
 ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGCATGTTTTTGCCTGAACTCATCCTGCTGCCAGTGTTAC
 TGGATTATTCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCAACAGGAGACGCGCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCTTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGATGAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAATAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGATCGGAACAACCTCACTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCTCTCAGCAGCGG
 TGAGACTCTCTCCTGTGTGTGCTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
 CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVEKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGAAAAACAATAAGCAAAGGAAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
GGATGAAGATGGATACATCACCTTAAATATTTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
TGAAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAAATGCACCTACCTTCTGTG
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVVKQSELKGTFKGHKCSPCDINWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP



FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCCGATCCCCGG
 CCGGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCCAGTTCGGAGAA
 GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGCAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCGGGTCAAACCTTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACCTGTACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCAGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
 GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAAGTACATTTACCAACAAACAGG
 CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACTGGG
 CAACCTGGATATTCTGAGACATATTTGGGGGGATTTTCAGTGAAAAAAGTGGGGGATCCCC
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGCTCTTGAAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGG
 CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTGTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGGCGCCCGCGCGGCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCAACCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGAGTCTCTACAGTTGCGCCGATTTACAGCTGAGTGTGCGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCTATGAAGGGAACCGAGTTAAGAAGACAA
 GGAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIQKREVREPGGSRPVSAQRRVCPRGTSKSLCQQLLLLLSKVRLCGGRPARPDR
GPEPQLKGIIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBCF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAACCAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRRLR
 RQDPQLKGIVTRLYCRQGYLQMHDPDGDGTDKDDSTNSTLFLNLPVGLRVVAIQGVKTGLY
 IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
GAAGGATGCAGGACGACGCTTTCTCCTGGAAACGAAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCAATCAAGAAATG
AAATAAACAGAGTTAGACCCGCGGGGGTGGTGTGTCTGACATAAAATAAATAATCTTAAGCAGCTGTTCC
CTCCCCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGAGTTACAAAGAAAAAAGTATGTTCAATTT
TTCTCTATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTTGGAATGAAAAGTTGGGGCTTTTTAGTAAAGTAA
AGAAGTGGTGGTGGTGGTTTTCTTTCTTTTTGAATTTCCCAAGAGGAGAGAAATTAATAATACATCTGC
AAAGAAATTTAGAGAAAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA
CAGTTGGATTGTGCTATGTTGACTAAATGACGGATAATGCGATTGGATTTTTCTTCATCAACCTCCTTT
TTTTTAAATTTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTTAACCACTGGATTCCATCT
GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAGGACCAACACAGATAAATTTATGAATG
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTTAACAGGGCCCTATTGTACCCCT
GCTGTGGTGTGCTGGCTCTTCAACTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
GCTCTGCAGCAACCAAGTTAGCAAGGTGATTTGTGTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAAGTGAACAGCTTCAAGCACTTGAG
GCAGTTGAAAATCCTACAGTTAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTCAATGGTCTGGCGA
ACCTCAACACTCTGGAACCTTTGACAACTCGTCTTACTACCATCCGAATGGAGCTTTTGATACTGTCTAAA
CTGAAGGAGCTCTGTTGCGAAACACCCCAATTGAAAGCATCCCTCTTATGCTTTTAACAGAAATTCCTTCTTT
GCGCCGACTAGACTTAGGGGAATTTGAAAGACTTTTACATACATCTCAGAAGTGCCTTTGAAGTCTGTCCAAT
TGAGTATTTGAACTTGGCATCTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAG
CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCGCTCTTCCAGGGTTTGATGCACCTTCAAAAAT
GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA
ACCTGGACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
TTACATCACACCCCTTGAAGCTGTAACCTGTGACATACTGTGGCTCAGTGGTGGATAAAAGACATGGCCCTC
GAACACAGCTTGTGTGCCCCGGTGAACACTCCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGATGGCAGCT
GAGCTGAAATGTGCGGCCCTCCACATCCCTGACATCTGTATCTTGATTACTCCAAATGGAACAGTCATGACACA
TGGGGCGTACAAAGTGGCGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATA
CAGGCATGTACACATGATGTGTGAGTAATTCGTTGGGAATACTACTGCTTCAAGCCCTGAAATGTTACTGCA
GCAACCACTACTCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
GACCACAGATAACAATGTGGGTCCTCACTCCAGTGGTGCAGCTGGGAGACCACCAATGTGACCACCTCTCTCAC
CAGAGAGCACAAGGTCGACAGAGAAAACCTTACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAAT
GATGAGTCTATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACATCATGGCTGCAGTGATGCT
GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAGGACTGTTGAAATTA
TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGGCCACTGCCATGCCTGCTATCGAGCATGAG
CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAAACACAATAAATCTCAATACA
CAGTTTCAGTGATGAACCGTATTGATCCGAATGAACCTCTAAAGACAATGTACAAGAGACTCAAACTCTAAACA
TTTACAGAGTTACAAAAAACAACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
ATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAAGAAAGAAATTTATTTATTAATAATCTATTG
TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKM TLHPQQIMIGPFRNRLFDP LLVLLALQLLVVAGLVRAQTCP SVCSCSNQFSKVIC
 VRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGLGELKRIS
 YISEGAFEGLSNLRYLNLAMCNLREIPNLTP LTKDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHPWNCNC DIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGT LNFNTVTVQDTGMYTCMVNSVGN
 TTASATLNVAATTT PFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRQHHRQN
 HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCGGGGAGCCCATCTGCCCCAGGGGACGGGGCGGGGCGGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA
 GCGCGCCGCGCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCGCGTCCGGGGATC
 GGG**ATG**TCCTCTCCTCTCTCCTCTTGCTAGTTTCC**TACTAT**GT**TGGA**ACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCTGCCACCATCACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAAGGCCG
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAAATCAGGGCCGTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGAGTGATCATCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT
 GACTACAACCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGACAGT
 ATGTACAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCTCCACTCGCTCCACAGCAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCGAGCCAGAGCAGAGCCTTCCAA
 ACGGTCT**TGA**ATTACAATGGACTTGACTCCACGCTTTCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCAACAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTAGATGAGCATTTTCTTATACAATACCAACAGCAAA
 AGGATGTAAGCTGATTATCTGTAAAAAGGCATCTTATTGTGCCCTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTGAGGGAAAGGTG
 AGGTGAATATACCTAAAACTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAAATT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTCAGACAGTCAAGCAGAACCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGCTCTTCTATTCTGACTTAAC
 TTCATTTGTCTAAAGGTTTGATATTAATTTCAAGGGGAGTTGAAATAGTTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAACTCTACTATTTGATTAGGCCCAAAATAAC
 TATGAAAGGAGACAAAAATTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCTCATGATT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTTCAAA
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTCTGGAAGGAGAAAAACAACATGTCAATT
 TATCAAGCTCTTTAGAAAGAAATTTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCAACATACCATTATAGTCTCTTCTTTCTGAGAAAAATGTGAACAGGATTCGAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTCCAGGCACCTGTAGGAATAACAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACCTCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGGGGGAGCCTGGGACCAGGAGCGAGGCCCTACCTGCAGCGCGCGCCACGGCAGCGCAGCCA
 CCA**ATG**GGCGCTCCTGCTGTGCTCTGCTCTGTGCGGAGTAGTGGATTTCCGCCAGAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAAAGGCCAAAGGGGAAACTGCCATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGAGCCGCTGACATCCAGTGCTGATATCACCAGCTGATATCAGAAGGTGGATCAAGTGATTATTTAT
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTAGATTTTACGAGTAATGATCTC
 AAATCTGGTGATGATCAATAAATGTAAACGAATTTACAACCTGTCAGATATTGGCACATATCACTGCAAGGTGAA
 AAAAGCTCCTGGTGTGCAAAATGAAGATTCATCTGGTAGTCTTGTTAAAGCTCTCAGTGCGAGATGTTGAC
 TTGATGGATCTGAAGAAATTTGGAGTGACTTTAAGATAAAATGTGAACCAAAGAGGTTCACTTCCATTACAG
 TATGAGTGGCAAAATTTGCTGACTCACAGAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTA AAAAATGCCTCTCTGAGTACTCTGGACATACAGCTGTACAGTCAGAAACAGATGGGCTCTGATC
 AGTGCTCTGTGCTCTAAACGTTGTCCTCTCTCAAATAAAGCTGGACTAATTCAGAGAGCCATTATAGGAAT
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTTGCTGTGTA AAAAGCGCAGAGAGA AAAAATATGAAA
 GGAAGTTTCATCAGATATCAGGGAAGATGTGCCACCTCCAAGAGGCGTAGCTCCATGCCAGAGCTACATCG
 GCAGTAATCATTATCCTGGGGCCATGCTCCTTCCAACATGGAAGGATATCCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCCTCAGATCCGACTCTCCACCTGCTAAGTTCAAGTACCCTTACAA
 GACTGATGGAATTACAGTTGTAT**TAA**ATATGGACTACTGAAGATCTGAAGTATTGTATTATTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTATGCAATGGCATTTAGACATGTAAGTCAGATGTCATGTCAAATTAGTACGAGCCAATTCCTTGT
 TAAAAAACCTATGTATAGTACACTGATAGTTAAAGATGTTTTATATATTTCAATAACTACCACATAACAA
 ATTTTAACTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAAATGTTGATTTTCAA
 AGGAATTTTAAATTTCTACGTTCTGTTAATGTTTTTGCTATTAGTTAAATACATTGAAGGGGAATACCCG
 TTCCTTTCCCTTTTATGCACACAACGAAACACGCGTTGTCATGCGCTCAAACATTTTTTTATTTGCAACTACA
 TGATTTACACAAATCTCTTAAACAACGACATAAAATAGATTTCCTTGATATAATAAATCTACATACGCTCCA
 TAAAGTAATTTCTCAAAGGTGTGAGAACAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATAAATATCAAGTCCAATATAAAAACTTAGGCATCTGACTAATTTTATAAAATTTCTCAAACATA
 TATCAATATCAAGTGCATATATTTTAAAGAAAGATTATTCTCAATAACTCTATAAAAAATAAGTTTGATGG
 TTTGCCCATCTAAGTTCACATCTATTAGTAGAAGCTTTTAACTTTTAAATGTGTAGTAAGGTTTATCTACCTT
 TTTCTCAAGATGACACCAACACAAATCAAAAACGAAGTAGTGAGGTCTAAGATGTGAGGATTAAATCCAGTGT
 TCCGGTCACATGCAATCCAGAGGAGGTACCAATGTCACTGGAATTTGGCGATATGGTTTATTTTCTTCCC
 TGATTTGGATAACCAATGGAACAGGAGGAGTATGATCTCTGATGGCCATTCCCTCGTATCATTCTCTGGCTT
 TTTTCTGGGCAAGGGTGCCACATTCGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACAT
 TAAGTTTATTCAAAGGAAAAATCATCATCTATGTTCCAGATTCTCATTTAAAGACAAAGTTTACCACAACAT
 GAGATCACATCTAAGTGCACTCCTATTGTCAGGTCTAATAACATTA AAAACCTCATGTATATAGCGGTATAA
 TGTATAACAGGTGACCAATTTTTCTGAATGCATAAAGAAATGAATAAATCAACACAGTCTCTTAAACAA
 CTTCAACCAAAAAGACCAAAACATGGAACGAATGGAAGCTTGTAAGGACATGCTTTTGTAGTCCATGGTTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCTATATCTCT
 AGCAAACTAATGCAGAAACGAAAAATCAACTACCGCATCTCTCACTTTAAGTGGAGGTATGATGAAGAAT
 TATGACACAAGAGAGGAACATAGACATTGGAGTCTATTTGAGAGGGGGGGTGGGAGAGGAAAGGAGCA
 GAAAGATTAATTTAGTAGTCTGCTTCAACCTGGGTGATGAATAATATATCTGCAACAATCTCTCTGTGACACA
 GTTTTACCTATGGAACAAACCTTCATGTGATCCCTAAACCTAAATATAAGTTTAAAAA AAAAAAAAAAAAAA
 AA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPD LKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVSGDQCLRLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKVEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSED FERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCGCTCTGATTGGTGA
 ATGGTGAAGGTGCGCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCGCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCGCTGGGTTTTACCCGTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATCTCTACTCTGGCCAACAACAT
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACAGGCGGTTCCTGCTATTCCGGAGAGCATTCAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGGACTGGTTTGTTCCTGTGTCATTTCA
 AACAGTCTCCCTTCCATGCTGTTCACTGGGACACTTCACGCCCTTGCCATGGGTCCCATTCT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTATTTT
 AATTAATGTCAGTATTTCAACTGAAGTTCATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCCTTTTTTTTT
 TATCCTAGTCATTCTTCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQLQLSLWTLARPFPCPLLATASQMQMVVLPCLGFTLLLSQVSGAQGGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

TOFT-BEUGO

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGCTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAAGGGGAAGGAGATGGGGAAGGCCCTTGACGTGAAAGTCC
CACTGGCTGGCTCAGGCTGTCTTATCCGCTTGAAAATAGGCAGGAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAAATCCATATTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMOKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACCGGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCGCTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGATGTTGGGGGCCGCGCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCTCTCCCACTGCTCGGCTCCAGTGGGGTGGCCTGATCCACCTGTACACAGGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACTCTGCATGGATTTTCAGAGGCAACATTTTGGATCACACTATTTTCGAC
CCGGAGAAGTGCAGGTTCCAACACAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
TCAGTATCACTTCTTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTTCCAGGCATGAACC
CACCCCCGTACTCCAGTTCTCTGTCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACT
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGGAGACCCCTGAAGCT
GCTGAAGCCCCGGGCCGGATGACCCGGCCCCGGCCTCTCTGTTACAGGAGGATCCCGAGCG
CCGAGGACAACAGCCGATGGCCAGTGAACCATTAGGGTGTTGAGGGGCGGTTCAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHYLTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRRNEIPLIHENTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTCTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGCCCCAGCACCCGCGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGCCAGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCGCTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCGTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAATTCACAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTTGGAAGAAACCTCAGCCCTCTCTGTTGAGACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAATTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTCAGAGACACCGACCATTGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCTT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCAGACTGCCCGGAC
 GAGGCCGACCACAGAC**TGA**GTGCAGGTGAAATGGAGGTTCTCTCTCTGCGGTGAGTG
 TGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCACGCGCTCACTTCAGGTCTCCTTACTGCGTGTGAGGAGGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGATGTATGGGGAGGGGCTTCACTGTCTCCAGAGGTGTCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCCATCTGTGTGCTTCCATCCTGCA
 TTAATAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGFPSTRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSFNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAIFDTLCTDDSSSEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTNI
 EVINCITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEFPSY
 VKVSGAAPVSIAGSAVGKTTSFAGSSASSYPSEAAALKNFTPSETPTMDIATKGPFPSTRD
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

CGCGAGCATCCGCTCGCGTCTCTGCCGAGACCCCGCGCGGATTTCGCCGGTCTCTCCGCGCG
GCGCGACAGAGCTGTCTCGACCTCGGATGGCAGCGGGCGCGGGGTCTCTCGAGCGCA
GAGAGAAATCTCATCTGCTGTCAGCGCTTTCTAAGCAAACTAAGACAGAGGGAGGATTAT
CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTCTCGGGGAGAGAGGAG
CTTGACTTTACATTTTGTAATAATTTGTTCTCTCGACATTAAGGCTGTCTGCTAGTCAGAAT
GCTTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCAAGGAATC
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGATTCGTAATATTCTTGCTGTTCAA
AAAAACAATATCCAGGGACAAGCATGTAACCTGATGATCTTCGACATCGAAAACAGCTA
GACAAACCAACTGCTACTATTTTCTGCTCCCAAGCAGGAAGCTGTCCATTGAAACAGCA
AAAGGCACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCCGAGGAAGATTTCTCTTACATGCGCCAAATTTTCAACAGCAGTCACTCCC
TAGCCCATCATCACAGATATTCAAAGCCACCGATATCTCATGAGAGACACATTTCT
CAGAAGTTTGGATCTCTCAGATCAACCTGGAGAAACTATTTAAGATGGTAGAAGCAAGTGCCCA
GCTCCTTGCTTTAAGGAAAAAGGCCATCTCAGAGTTCACAAATTTTCTCTGATCAAGAA
TAGCTCATCTGCTGCTGAAAAATGTAGTGCCTGCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACTCTCGGCTACTCCAAGCCGCCACCTTTCTACCCCAATGCTTCAGTGACACC
TCTCTGGAGTTCTCCAGCCACAGCTGGCCACAGCTCCACTGTAACTACTGTCACTTCTC
AGCTCTCCACGACCTTCTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACCAACAGCAGTTCTGACTACCACTTTCCAGGCATACGGAATCGAAAGCGAGCTTGA
AACCATACCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTAATAACCTA
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGT
AGGAGAGCGAGCTCCAGGCAGTCTCTCCAGGCGAGTGTCTCAGAAAAATCATGACGCCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCGTCTCTTGSTGCTTCTGCTCTGGTATGAGCC
TCGTCCTCTCTGGGTAGAACTCTTTCCGAATCACTCCGACGGAACACTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAATCGGTGTCTCTTAATTCATT
TAGTAACGAGAAGCCCAATGCAATGAGTTTCTGCTGACTGCTAGTCTTAGACGAGGTTG
TATTTTGAAGACAGGAAATGCCCTTCTGCTTTCTCTTTTTTTTTTTTGGAGACAGAGTCTC
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCGCTCTC
CTGGGTTCAAGCAATCTTCTGCTCAGGCTCAAGTATCTGGAATCTGGAATACAGGCATGTGCCA
CCACACTCGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTACCATGTTGGTGCAGGCTC
GTCTCAAATCTCTGACCTAGTGATCCACCTCTCGGCTCCCAAAAGTCTGGGATTACAGG
CATGAGCCACACAGCTGGGCCCCCTCTGTTTTATGTTGGTTTTTGAGAAGGAATGAAGTG
GGAACCAAAATAGTAATTTTGGGTAAATGTCCTCAAATATTAAGTAAAAACAAAGCTCT
ATGTAAAGTAAATAAGTATAAATGTCATATAAATCTCAAATTAAGCTGGCTTTTATGAAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATCTTGGTTCCAGATAAAATCAAC
TGTTTATATCAATTTCAATGAGATTGCTTTTCTTTATATGGAATTCCTTTAAACTTAT
CCAGATGTAGTTCTCTCCAATTAATTTTGAATTAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVVICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIALLPENVSALPATVAVASPHHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTGGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCTCGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCTCTTCTCTCGTGCTCTGGCACCATTATGCAGAAGAAGGCGCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTTGGA
 ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGCTCCTCCCTCCCCCTTCTCCCAC
 CTTCACGCTCTGGCTACAACACGCTGACGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGGCCCTCCATTGCCAGGGACTTCCCAAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGACAGGGAGCTCCCGCCCCCATGTCAGC
 TGGACTCCACCTCAGCAGAGGACACCAAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCCTCTGTGTCAGC
 CGCAGGCCTGATCGCTTCTGACGCCACCTGCTCCTTGGGAGAAAAGGCTCAACAGGGCCA
 CGGAGACACAGAGAAACGAGAAGTTCTGGCTCTCAGCTTGACTGCGGAGGAAAAGGAAGCC
 CCTTCCAGGGCCCTGAGGGGGACGTGATCTGATGCCTCCCTCCACACATCTGAGAGGGA
 GCTGGGCTTCTCAGAATTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGCCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCATTCCCGAAAGCTTCCACCTCAGCCCTCAGAG
 TCAGCTGCCCGGACTCCAGGGCTCTCCCAACCTCCCGAGGCTCTCCTCTGCATGTTTCCA
 GCCTGACCTAGAAGCGTTTGTACGCCCTGGAGCCGACAGCGGTGGCCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGACAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCAGTGTGCGACCCTGCCCTCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGATGATTCCTGGCCCCACCAAGACCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCAGTGAAGTGTGCGACTTGAGTTTGGGGCCAGTGGGCGT
 ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCTGTGTAAG
 TCCAGGCTTTGGTCAAGTCAAGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCTTTNCCATTTGCCCTCCCTGNNCCATGCGCTTCTTGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGAAAGGGTTACTTGCCATGAGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTCCGAGAACGGGTCGGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTCTTTTCCATTATTTGTTTTTAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCTGGGTTCAAGTGAT
 CTCTGCCTCAGCCTCCCGAGTAGTGGGATTACAGGCACGACCACCACCTGGCTTAAT
 TTTGACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTCAGTCTCCCAAAATGCGGGATACAGGATAGGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAAAGTGAATTAAGAGTTGTTCAAGTATGCAAACTTGAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCACCCATAGCTTCACAGACACTGAT
 TATTTCTGTTTTGTTGTTACTTCTTCCACTCTTTTCTTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGAGCAATTTATCTGTATATACAACCTTTGATCCTGCTTTTCCACCTTATGCTCC
 ATCACTTTATCTCCAGCACTCTCTGTGTTTTACAGACCTTTTTATAAAATAAATGTTTATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCVGVEKRGPDSELLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEPPLPG
TSQYGHERTSQYTGTSPPHSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128